



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 150235

TO: Sumesh Kaushal  
Location: REM-2B85/2C70  
Art Unit: 1636  
Monday, April 11, 2005

Case Serial Number: 09/925674

From: Deirdre Arnold  
Location: Biotech-Chem Library  
REM 1A64  
Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

### Search Notes

**RUSH**

*Please feel free to contact me if you have any questions or would like to amend the search.*

Thank you for using STIC services.

Regards,  
Deirdre Arnold



***This Page Blank (uspto)***

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 14:45:43 ; Search time 3068.26 Seconds  
(without alignments)  
9206.966 Million cell updates/sec

Title: US-09-925-674B-6  
Perfect score: 583  
Sequence: 1 atggcgacccagcctcgcc.....cttttctgcaagtga 583

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_ats:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	583	100.0	583	6 AX022529	AX022529 Sequence
2	583	100.0	583	6 AX030817	AX030817 Sequence
3	577.2	99.0	582	6 AX481423	AX481423 Sequence
4	577.2	99.0	582	9 HSUS9747	US9747 Human Bcl-w
5	575	98.6	3542	9 D87461	D87461 Homo sapien
6	572.4	98.2	582	6 CO730429	CO730429 Sequence
7	567.8	97.4	579	6 AR020780	AR020780 Sequence
8	527.6	90.5	582	10 AF096291	AF096291 Rattus no
9	527.6	90.5	1110	10 AY185100	AY185100 Rattus no
10	527.6	90.5	3487	10 AY185098	AY185098 Rattus no
11	527.6	90.5	3545	10 BC074021	BC074021 Rattus no
12	523	89.7	579	6 AR020779	AR020779 Sequence
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14	522.8	89.7	3476	10 AF030769	AF030769 Mus muscu
15	511.8	87.8	3442	10 AK172925	AK172925 Mus muscu
16	510	87.5	3473	10 AY170344	AY170344 Mus muscu
17	501	85.9	581	6 AX022531	AX022531 Sequence
18	501	85.9	581	6 AX030819	AX030819 Sequence
19	441.2	75.7	220818	2 AC128940	AC128940 Rattus no

20	441.2	75.7	223933	2 AC097389	AC097389 Rattus no
21	424	72.7	1098	6 AR432565	AR432565 Sequence
22	424	72.7	1098	6 BD078624	BD078624 Human pro
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30	381.8	65.5	263901	2 AC115371	AC115371 Rattus no
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44	150	25.7	150	6 CQ203800	CQ203800 Sequence
45	150	25.7	150	6 CQ227167	CQ227167 Sequence

ALIGNMENTS

RESULT 1	AX022529	583 bp	DNA	linear	PAT 07-SEP-2000
LOCUS	AX022529	Sequence 6 from Patent EP0932674.			
DEFINITION	AX022529				
ACCESSION	AX022529.1	GI:10046125			
VERSION					
KEYWORDS	unidentified				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1				
AUTHORS	Adams, J.M., Holmgren, S.P., Cory, S. and Gibson, L.M.				
TITLE	A novel mammalian gene, bcl-2, belongs to the bcl-2 family of				
JOURNAL	apoptosis-controlling genes				
FEATURES	Patent: EP 0932674-A 6 04-AUG-1999;				
source	AMRAD OPERATIONS PTY LTD (AU)				
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ORIGIN					
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Best Local Similarity	100.0%;	Pred. No. 3.5e-121;			
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QY	61 AAGCTGAGGACGAGAGGTTATCTGTGAGCTGGCCCCGGGAGGAGCCACAGACTGAC	120			

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Db 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA 360  
QY 361 CAAGTCAGAGATGATGTGCTGCTTACCTGAGAGCGCGCTGCTGCACTGATCCACAGC 420  
Db 361 CAAGTCAGAGATGATGTGCTGCTTACCTGAGAGCGCGCTGCTGCACTGATCCACAGC 420  
QY 421 AGTGGGGCTGGGCGGAGTTCAAGCTCTATACGGGGAAGGGGCGCTGAGAGAGCGCGG 480  
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QY 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTCTAGCAAGTGAA 583  
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RESULT 2  
AX030817 583 bp DNA linear PAT 20-SEP-2000  
LOCUS Sequence 6 from Patent WO9735971.  
DEFINITION AX030817  
ACCESSION AX030817  
VERSION AX030817.1 GI:10278311  
KEYWORDS  
SOURCE  
ORGANISM  
unidentified  
unidentified  
unclassified.

REFERENCE 1  
AUTHORS Adams, J.M., Holmgren, S.P., Cory, S. and Gibson, L.M.  
TITLE A novel mammalian gene, bcl-2, belongs to the bcl-2 family of  
JOURNAL apoptosis-controlling genes  
ADAMS JERRY MCKEE (AU) ; HOLMGREN SHAUN P (AU) ; CORY SUZANNE (AU)  
; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)  
LOCATION/Qualifiers

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CDS

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Query Match 100.0%; Score 583; DB 6; Length 583;  
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QY 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTCTAGCAAGTGAA 583  
Db 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTCTAGCAAGTGAA 583

RESULT 3  
AX481423 582 bp DNA linear PAT 16-AUG-2002  
LOCUS Sequence 37 from Patent WO02055693.  
DEFINITION AX481423  
ACCESSION AX481423  
VERSION AX481423.1 GI:22316337  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Kreutzer, R., Limmer, S., Rost, S. and Hadwiger, P.  
TITLE Method for inhibiting the expression of a target gene  
JOURNAL Patent: WO 02055693-A 37 18-JUL-2002;  
Ribopharma AG (DE)  
LOCATION/Qualifiers

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ORIGIN

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QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGTGCGAGACTTGTAGTTAT 60  
Db 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGTGCGAGACTTGTAGTTAT 60  
QY 61 AAGCTGAGGAGAGAGGTTATGTCTGTGAGAGCTGGCCCCGGGAGAGGCCAGAGCTGAC 120  
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Db 61 AAGCTGAGCAGAAAGGGTTATGTCTGTGAGCTGGCCCCGGGAGAGGCCCAACAGACTGAC 120

QY 121 CCGCTGCACCAAGCCATGCGGCGAGCTGGAGATGAGTTGAGACCCGCTTCCGGCGACC 180

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QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGAACCCAGGCTCAGCCCAAGCAACGCTTACC 240

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QY 241 CAGGCTCCGACGAACCTTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCCTTCTTT 300

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QY 541 GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAGTGA 582

Db 541 GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAGTGA 582

RESULT 4

LOCUS HSU59747 582 bp mRNA linear PRI 29-SEP-1996

DEFINITION Human Bcl-w (bcl-w) mRNA, complete cds.

ACCESSION U59747

VERSION U59747.1 GI:1572492

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 2 (bases 1 to 582) 3 Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. bcl-w, a novel member of the bcl-2 family, promotes cell survival Oncogene 13 (4), 665-675 (1996)

TITLE JOURNAL MEDLINE PUBMED 96358615 8761287

REFERENCE 2 (bases 1 to 582) 3 Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and Cory, S. Direct Submission Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia

FEATURES

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Query Match 99.0%; Score 577.2; DB 9; Length 582;  
Best Local Similarity 99.5%; Pred. No. 7.2e-120;  
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGCGAACCAGCCTCGGCCCAACACACAGGGCTCTGTGGCAGACTTTGTAGTTAT 60

Db 1 ATGCGAACCAGCCTCGGCCCAACACACAGGGCTCTGTGGCAGACTTTGTAGTTAT 60

QY 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGAGCTGGCCCCGGGAGGGCCCAAGAGCTGAC 120

Db 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGAGCTGGCCCCGGGAGGGCCCAAGAGCTGAC 120

QY 121 CCGCTGCACCAAGCCATGCGGCGAGCTGAGATGAGTTGAGACCCGCTTCCGGCGACC 180

Db 121 CCGCTGCACCAAGCCATGCGGCGAGCTGAGATGAGTTGAGACCCGCTTCCGGCGACC 180

QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGAACCCAGGCTCAGCCCAAGCGCTTACC 240

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QY 241 CAGGCTCCGACGAACCTTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCCTTCTTT 300

Db 241 CAGGCTCCGACGAACCTTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCCTTCTTT 300

QY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAACCACTGTGGGA 360

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Db 361 CAAGTGCAGAGTGTGATGTGGCTTACCTTGAGACGGGCTGTGACTGATCCACAGC 420

QY 421 AGTGGGGGCTGGCGGAGTTCAACAGCTCTATACGGGGACGGGGCCCTGAGAGAGCGCGG 480

Db 421 AGTGGGGGCTGGCGGAGTTCAACAGCTCTATACGGGGACGGGGCCCTGAGAGAGCGCGG 480

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Db 481 CGTCTGGGGAGGGGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCCCTGGCACTG 540

QY 541 GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAGTGA 582

Db 541 GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAGTGA 582

RESULT 5

LOCUS D87461 3542 bp mRNA linear PRI 10-JAN-2004

DEFINITION Homo sapiens mRNA for KIAA0271 gene, partial cds.

ACCESSION D87461

VERSION D87461.1 GI:1944417

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 2 Nagase, T., Seki, N., Ishikawa, K., Ohira, M., Kawarabayashi, Y., Ohara, O., Tanaka, A., Kotani, H., Miyajima, N. and Nomura, N. Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain DNA Res. 3 (5), 321-329 (1996)

TITLE JOURNAL MEDLINE 97191544

PUBMED 9039502  
REFERENCE 2 (bases 1 to 3542)  
AUTHORS Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.  
TITLE Direct Submission  
JOURNAL Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute;  
1532-3, Yana, Kisarazu, Chiba 292-0812, Japan  
(E-mail:cdnaifco@kazusa.or.jp, Tel:+81-438-52-3913)

FEATURES  
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ORIGIN

Query Match 98.6%; Score 575; DB 9; Length 3542;  
Best Local Similarity 99.1%; Pred. No. 1.8e-119;  
Matches 578; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
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QY 541 GGGGCCCTGTGTAAGTGTAGGGCCTTTTGTGCTAGCAAGTGAA 583  
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RESULT 6  
CQ730429  
LOCUS CQ730429 582 bp DNA linear PAT 03-FEB-2004  
DEFINITION Sequence 16363 from Patent WO02068579.  
ACCESSION CQ730429  
VERSION CQ730429.1 GI:42304244  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Venter,C.U., Adams,M.C., Li,P.W. and Myers,E.W.  
TITLE Kils, such as nucleic acid arrays, comprising a majority of  
humanexons or transcripts, for detecting expression and other uses  
thereof  
JOURNAL Patent: WO 02068579-A 16363 06-SEP-2002;  
PE Corporation (NY) (US)

FEATURES  
source  
1.582  
Location/Qualifiers

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ORIGIN

Query Match 98.2%; Score 572.4; DB 6; Length 582;  
Best Local Similarity 99.0%; Pred. No. 8.8e-119;  
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RESULT 7
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ACCESSION AR020780
VERSION AR020780.1 GI:3975395
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 579)
TITLE Guastella,J.
JOURNAL Genes coding for bcl-y a bcl-2 homologue
Patent: US 5789201-A 2 04-AUG-1998;
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Best Local Similarity 98.8%; Pred. No. 9.6e-118;
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AF096291 LOCUS
DEFINITION Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION AF096291
VERSION AF096291.1 GI:3747129
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KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 582)
AUTHORS Hamner,S., Skogjosa,Y. and Lindholm,D.
TITLE Differential expression of bcl-w and bcl-x messenger RNA in the
developing and adult rat nervous system
JOURNAL Neuroscience 91 (2), 673-684 (1999)
MEDLINE 99292146
PUBMED 10366024
REFERENCE 2 (bases 1 to 582)
AUTHORS Hamner,S., Skogjosa,Y. and Lindholm,D.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala
University, Box 587, BMC, Uppsala 751 23, Sweden
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ORIGIN
Query Match 90.5%; Score 527.6; DB 10; Length 582;
Best Local Similarity 94.2%; Pred. No. 1.1e-108;
Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1 ATGGGACCCCAAGCTTCGGCCCCAGACACAGGGCTCTGGTGACAGCTTTGTAGTTAT 60
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QY 61 AAGCTGAGGACAGAGGGTTATGTCTGTGAGAGCTGGCCCCGGGGAGGGGCCCAAGCTGAC 120
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DEFINITION  
ACCESSION AY185100  
VERSION AY185100.1 GI:32185284  
KEYWORDS  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus

REFERENCE  
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.  
TITLE Bcl-2-related protein family gene expression during  
oligodendroglial differentiation  
JOURNAL J. Neurochem. 85 (6), 1500-1512 (2003)  
MEDLINE 22672518  
PUBMED 12787069

REFERENCE  
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.  
TITLE Direct Submission  
JOURNAL Submitted (21-NOV-2002) Neurology Research, The Children's Hospital  
of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center  
Blvd., Philadelphia, PA 19104, USA

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CDS

ORIGIN

Query Match 90.5%; Score 527.6; DB 10; Length 1110;  
Best Local Similarity 94.2%; Pred. No. 1e-108;  
Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCAAGCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGTTAT 60  
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ACCESSION AY185098  
VERSION AY185098.1 GI:32185280  
KEYWORDS  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus

REFERENCE  
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.  
TITLE Bcl-2-related protein family gene expression during  
oligodendroglial differentiation  
JOURNAL J. Neurochem. 85 (6), 1500-1512 (2003)  
MEDLINE 22672518  
PUBMED 12787069

REFERENCE  
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.  
TITLE Direct Submission  
JOURNAL Submitted (21-NOV-2002) Neurology Research, The Children's Hospital  
of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center  
Blvd., Philadelphia, PA 19104, USA

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QY 61 AAGCTGAGGACAGAGGGTTATGTCTGTGAGCTGCCCCGGGGAGGGCCAGCAGCTGAC 120  
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DB 410 CAGGTTCCGACGAATTTTTCAGAGGGGGCCCCAATGGGGCCGCTTGTAGCCTTCTT 469  
QY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA 360  
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ACCESSION BC074021  
VERSION BC074021.1 GI:49256646  
KEYWORDS MGC.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 3545)  
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,  
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,  
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,  
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,  
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,  
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,  
Scheetz,T.E., Brownstein,M.J., Uedln,T.B., Toshiyuki,S.,  
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,  
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,  
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,  
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,  
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,  
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,  
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,  
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,  
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,  
Butterfield,Y.S., Krzywinski,M.T., Skalska,U., Smailus,D.E.,  
Schnerch,A., Schein,J.B., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
PUBMED 12477932  
REFERENCE 2 (bases 1 to 3545)  
AUTHORS Strausberg,R.  
TITLE Direct Submission  
JOURNAL Submitted (23-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
COMMENT Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Howard Jacobs  
CDNA Library Preparation: Express Genomics  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)  
Ahter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,  
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,  
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,  
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Latic,P., Legaspi,R.,  
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,  
McDowell,J., Pearson,R., Stantiripop,S., Thomas,P.J., Touchman,J.W.,  
Tsurgoun,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,  
Young,A., Zhang,L.-H. and Green,E.D.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>  
Series: IRAX Plate: 175 Row: P Column: 4  
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ORIGIN

Query Match 90.5%; Score 527.6; DB 10; Length 3545;  
Best Local Similarity 94.2%; Pred. No. 9e-109;  
Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;  
QY 1 ATGGCGACCCGAGCTCGGCCCCAGACACAGCGGCTCTGGTGAGACTTTGTAGTTAT 60  
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ACCESSION AR020779  
VERSION AR020779.1 GI:3975394  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 579)  
AUTHORS Guastella,J.  
TITLE Genes coding for bcl-y a bcl-2 homologue  
JOURNAL Patent: US 5789201-A 1 04-AUG-1998;  
FEATURES location/Qualifiers  
source 1..579  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 89.7%; Score 523; DB 6; Length 579;  
Best Local Similarity 94.0%; Pred. No. 1.2e-107;  
Matches 544; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCGCTGGCCCCAGACACACGGGCTGTGTGACAGACTTTGTAGTTAT 60  
Db 1 ATGGCGACCCCGCTCAACCCAGACACACGGGCTGTGTGACAGACTTTGTAGTTAT 60  
QY 61 AAGCTGAGCAGAGGGTTATGTCTGTGAGCTGGCCCCGGGAGGGCCCCAGCAGCTGAC 120  
Db 61 AAGCTGAGACAGAGGGTTATGTCTGTGAGCTGGCCCCGGGAGGGCCCCAGCAGCTGAC 120  
QY 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCCGCTTCCGGCGCAC 180  
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QY 181 TTCTTGATCTGGCGGCTCAGCTGATGTGACCCCAAGGCTCAGCCCAAGCAAGCCTTCA 240  
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QY 301 CTCTTTGGGCTGCACTGTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 360  
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QY 541 GGGGCCCTGTACTGTAGGGGCTTTTGTGCTAGCAAG 579  
Db 541 GGGGCCCTGTACTGTAGGGGCTTTTGTGCTAGCAAG 579

RESULT 13  
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DEFINITION Mus musculus Bcl-w (bcl-w) mRNA, complete cds.  
ACCESSION U59746  
VERSION U59746.1 GI:1572494  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 582)  
AUTHORS Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
TITLE Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Copeland,N.G.,  
Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.  
JOURNAL Oncogene 13 (4), 665-675 (1996)  
MEDLINE 96358615  
PUBMED 8761287  
REFERENCE 2 (bases 1 to 582)  
AUTHORS Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and  
Cory,S.  
TITLE Direct Submission  
JOURNAL Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and  
Eliza Hall Institute of Medical Research, PO Royal Melbourne  
Hospital, Parkville, Victoria 3050, Australia  
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Query Match 89.7%; Score 522.8; DB 10; Length 582;  
Best Local Similarity 93.6%; Pred. No. 1.4e-107;  
Matches 545; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCGCTGGCCCCAGACACACGGGCTGTGTGACAGACTTTGTAGTTAT 60

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Db 1 ATGGCGACCCGACCTCAACCCAGACACACGGGCTTAGTGCTGACTTTGTAGGCTAT 60  
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RESULT 14  
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LOCUS AF030769 Mus musculus BCL-W (Bcl-w) mRNA, complete cds.  
DEFINITION AF030769  
ACCESSION AF030769  
VERSION AF030769.1 GI:2623249  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 3476)  
AUTHORS Ross,A.J., Waymire,K.G., Moss,J.E., Parlow,A.F., Russell,L.D. and MacGregor,G.R.  
TITLE Bcl-w is required for testis homeostasis  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3476)  
AUTHORS Ross,A.J. and MacGregor,G.R.  
TITLE Direct Submission  
JOURNAL Submitted (21-OCT-1997) Center for Molecular Medicine, Emory University, 1462 Clifton Road, Atlanta, GA 30322, USA  
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Query Match 89.7%; Score 522.8; DB 10; Length 3476;  
Best Local Similarity 93.6%; Pred. No. 1.1e-107;  
Matches 545; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 ATGGCGACCCGACCTCGGGCCCAAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT 60  
Db 179 ATGGCGACCCGACCTCAACCCCAAGACACACGGGCTCTGTAGGCTAT 238  
QY 61 AAGCTGAGGCAGAAAGGTTATGTCTGTGAGAGCTGGCCCCGGGGAGGGCCCAAGCACTGAC 120  
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QY 541 GGGGCCCTGGTAACTGTAGGGGCTTTTGTCTAGCAAGTGA 582  
Db 719 GGGGCCCTGGTAACTGTAGGGGCTTTTGTCTAGCAAGTGA 760

RESULT 15

AK172925  
LOCUS AK172925 3442 bp mRNA linear ROD 28-JUL-2004  
DEFINITION Mus musculus mRNA for mKIAA0271 protein.  
ACCESSION AK172925  
VERSION AK172925.1 GI:50510434  
KEYWORDS FLI\_CDNA.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS 1 Okazaki,N., Kikuno,R.F., Ohara,R., Inamoto,S., Koseki,H., Hiraoka,S., Saga,Y., Seino,S., Nishimura,M., Kaisho,T., Hoshino,K., Kitamura,H., Nagase,T., Ohara,O. and Koga,H.  
TITLE Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene: IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous cDNAs Identified by Screening of Terminal Sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries  
JOURNAL DNA Res. 11, 205-218 (2004)  
REFERENCE 2 (bases 1 to 3442)  
AUTHORS Okazaki,N., Kikuno,R.F., Nagase,T., Ohara,O. and Koga,H.  
TITLE Direct Submission  
JOURNAL Submitted (19-MAY-2004) Hisashi Koga, Kazusa DNA Research Institute, Laboratory for Genome Informatics; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)  
COMMENT The CREATE program supported by Japan science and technology corporation; cDNA full insert sequencing: Kazusa DNA Research Institute; cDNA library construction, clone selection and 5'- & 3'-end one pass sequencing.  
FEATURES  
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Query Match 87.8%; Score 511.8; DB 10; Length 3442;  
Best Local Similarity 93.5%; Pred. No. 3.3e-105;  
Matches 545; Conservative 0; Mismatches 37; Indels 1; Gaps 1;  
QY 1 ATGGGACCCCGAGCCTCGGCCAGACACAGGGCTCTGTGGCAGACTTTGAGGTTAT 60  
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QY 61 AAGCTGAGGAGAGGGTTATGTCTGTGAGCTGGCCCCGGGGAGGGCCAGCAGCTGAC 120  
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QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGATTGAGACCGCGCTTCGGCGCAC 180  
DB 126 CCGCTGCACCAAGCCATGCGGGCTGCTGAGACGAGTTGAGACCGCGTTCCGCGCAC 185  
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCGACGACGCTTACC 240  
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QY 541 GGGGCCCTGTAACTGTAGGGCC-TTTTGTGCTAGCAAGTGA 582  
DB 546 GGGGCCCTGTAACTGTAGGGCCTTTGTGCTAGCAAGTGA 588

Search completed: April 10, 2005, 18:37:53  
Job time : 3078.26 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: April 10, 2005, 14:40:06 ; Search time 457.785 Seconds  
(without alignments)  
7538.927 Million cell updates/sec

Title: US-09-925-674B-6  
Perfect score: 583  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

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2:	geneseqn1990s:*
3:	geneseqn2000s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	583	100.0	583	2	AAx25134	Aax25134 Human bcl
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4	577.2	99.0	582	6	ABZ35729	Abz35729 Human bcl
5	577.2	99.0	582	6	ABX09972	Abx09972 Human bcl
6	577.2	99.0	582	6	ABL91694	Ab191694 Human pol
7	575	98.6	3542	8	ABT16642	Abt16642 Human bcl
8	573	98.3	581	2	AAx25132	Aax25132 Human bcl
9	567.8	97.4	579	2	AAV28334	Aav28334 Human bcl
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11	527.6	90.5	582	10	ADB52996	Adb52996 Primary r
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14	521.8	89.5	581	2	AAx25133	Aax25133 Mouse bcl
15	501	85.9	581	2	AAT96578	Aat96578 Mouse bcl
16	501	85.9	581	2	AAx25135	Aax25135 Mouse bcl
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18	424	72.7	1098	2	AAV41925	Aav41925 Nucleotid
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26	255.4	43.8	6049	6	ABL32228	Ab132228 Human imm
27	219.8	37.7	6049	6	ABL32229	Ab132229 Human imm
28	152	26.1	590	12	ACH80189	Ach80189 Human gen
29	151	25.9	151	12	ACH93889	Ach93889 Human gen
30	150	25.7	150	4	AAI20236	Aai20236 Probe #10
31	150	25.7	150	4	ABA65269	Abas65269 Human foe
32	150	25.7	150	4	AAI45438	Aai45438 Probe #14
33	150	25.7	150	4	ABA47382	Abas47382 Human bre
34	150	25.7	150	4	ABA32370	Abas32370 Probe #10
35	150	25.7	150	4	AAK39424	Aak39424 Human bon
36	150	25.7	150	4	AAK13683	Aak13683 Human bra
37	150	25.7	150	4	ABS39016	Abs39016 Human liv
38	150	25.7	150	5	AAT05940	Aat05940 Probe #59
39	150	25.7	150	6	ABS13513	Abs13513 Human gen
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42	143	24.5	1742	4	AAF75960	Aaf75960 Rat wild-
43	141.2	24.2	540	12	ADH52634	Adh52634 Chinese h
44	138.2	23.7	702	13	ADQ80676	Adq80676 Rat anti-
45	138.2	23.7	5903	13	ADQ80674	Adq80674 Bcl-XL ex

ALIGNMENTS

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ID	AAT96577 standard; DNA; 583 BP.
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AC	AAT96577;
XX	
DT	22-APR-1998 (first entry)
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DE	Human bcl-w DNA.
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KW	Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW	diagnosis; degenerative disease; ss.
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PD	02-OCT-1997.
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PF	27-MAR-1997; 97WO-AU000199.
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PR	27-MAR-1996; 96AU-00008965.
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PA	(AMRA-) AMRAD OPERATIONS PTY LTD.
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PI	Cory S, Adams JM, Gibson LM, Holmgreen SP;
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DR	WPI; 1997-489635/45.
DR	P-PSDB; AAW36047.
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PT	Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
PT	inhibit cell survival, e.g. for treatment of cancer and degenerative
PT	diseases.
XX	
PS	Claim 3; Page 48; 86pp; English.
XX	
CC	This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene
CC	family, extracted from an adult brain library. This gene promotes cell



CC survival, so its modulation is useful in treatment of cancer or auto-  
CC immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease,  
CC myocardial infarct, muscular degeneration, hypoxia, ischaemia, human  
CC immunodeficiency virus infection or in cell transplants. Up-regulation of  
CC the gene can also be used to modify cell lines cultured in vivo, e.g. to  
CC develop new lines, to facilitate isolation of hybridomas and to increase  
CC survival of primary explants during genetic modification. It can be used  
CC to produce recombinant Bcl-w for therapy, diagnosis, antibody production  
CC or screening of potential modulators  
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Query Match 100.0%; Score 583; DB 2; Length 583;  
Best Local Similarity 100.0%; Pred. No. 1e-135;  
Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGCGCTCTGTGGCAGACTTTGTAGTTAT 60  
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DB 421 AGTGGGGGCTGGGCGAGTTCACAGCTCTATACGGGAGCGGGCCCTTGAGAGAGCGCG 480  
QY 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCGCTGGCACTG 540  
DB 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCGCTGGCACTG 540  
QY 541 GGGGCGCTGTACTGTAGGGGCTTTTGTGCTAGCAAGTGA 583  
DB 541 GGGGCGCTGTACTGTAGGGGCTTTTGTGCTAGCAAGTGA 583

RESULT 2

AAK25134  
ID AAK25134 standard; DNA; 583 BP.  
XX  
AC AAK25134;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Human bcl-w gene derivative.  
XX  
KM Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;  
XX animal model; ss.  
OS Homo sapiens.  
XX  
PN WO9913710-A1.

XX  
PD 25-MAR-1999.  
XX  
PF 16-SEP-1998; 98WO-AU000764.  
XX  
PR 16-SEP-1997; 97AU-00009228.  
XX  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX  
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;  
XX  
DR WPI; 1999-243890/20.  
DR P-PSDB; AAY05532.  
XX  
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
XX protein associated with Bcl-w.  
XX  
PS Disclosure; Page 36; 52pp; English.  
XX

CC The present sequence is described as a derivative of the human bcl-w gene  
CC (see AAK25132) and encodes Bcl-w protein (see AAY05532), a pro-survival  
CC member of the Bcl-2 family which is widely expressed and which is  
CC essential for spermatogenesis. The invention relates generally to a  
CC method of treatment and to an animal model for the identification of  
CC molecules and genetic sequences useful for inducing or reducing fertility  
CC of male animals. Methods are provided for the treatment of infertility,  
CC or for reducing fertility, by modulating spermatogenesis. An animal model  
CC carries a mutation is at least one allele of the human or murine bcl-w  
CC gene or in a gene associated with bcl-w. Such animals have disorganised  
CC seminiferous tubules and are substantially infertile, but possess no other  
CC major abnormalities as determined by histological examination. They can  
CC be used to screen for therapeutic molecules including genetic sequences  
CC capable of inducing, enhancing or otherwise facilitating spermatogenesis  
CC in animals, or which can induce infertility  
XX

SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;

Query Match 100.0%; Score 583; DB 2; Length 583;  
Best Local Similarity 100.0%; Pred. No. 1e-135;  
Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACGCGCTCTGTGGCAGACTTTGTAGTTAT 60  
DB 1 ATGGCGACCCAGCCTCGGCCCCAGACACGCGCTCTGTGGCAGACTTTGTAGTTAT 60  
QY 61 AAGCTGAGCAGAGGTTATGTCTGTGAGCTGCCCCGGGAGGCCCCAGAGCTGAC 120  
DB 61 AAGCTGAGCAGAGGTTATGTCTGTGAGCTGCCCCGGGAGGCCCCAGAGCTGAC 120  
QY 121 CCGTGACCAAGCCATGCGGCGAGCTGAGATGAGTTGAGACCCGCTTCCGCGCAC 180  
DB 121 CCGTGACCAAGCCATGCGGCGAGCTGAGATGAGTTGAGACCCGCTTCCGCGCAC 180  
QY 181 TTCTGTATCTGGGGCTCAGCTGATGAGACCCCAAGCTCAGCCAGCAACGCTTACC 240  
DB 181 TTCTGTATCTGGGGCTCAGCTGATGAGACCCCAAGCTCAGCCAGCAACGCTTACC 240  
QY 241 CAGTCTCCGACGAACCTTTTCAAGGGGGCCCCCACTGGGGCGCTTGTAGCTTTT 300  
DB 241 CAGTCTCCGACGAACCTTTTCAAGGGGGCCCCCACTGGGGCGCTTGTAGCTTTT 300  
QY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGA 360  
DB 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGA 360  
QY 361 CAAGTGACAGAGTGTGATGTGGCTTACCTGAGACGCGGCTGTGACTGATCCACAGC 420  
DB 361 CAAGTGACAGAGTGTGATGTGGCTTACCTGAGACGCGGCTGTGACTGATCCACAGC 420  
QY 421 AGTGGGGGCTGGGCGAGTTCAAGCTCTATACGGGAGCGGGCCCTGGAAGAGCGCG 480  
DB 421 AGTGGGGGCTGGGCGAGTTCAAGCTCTATACGGGAGCGGGCCCTGGAAGAGCGCG 480





CC with a double-stranded (ds) structure of at most 49 sequential nucleotide  
CC pairs. At least part of one strand (S1, S2) of the ds structures in each  
CC of dsRNAI and II are complementary to regions in the target gene. The  
CC method uses antisense inhibition of gene expression using double stranded  
CC RNA inhibition (RNAi). The method is particularly used to treat tumors  
CC or infections, especially by Plasmid or viruses/viroids (pathogenic on  
CC humans, animals or plants). The method provides more effective inhibition  
CC of expression than known methods using a single dsRNA, even at very low  
CC concentrations. When dsRNA has at least one unpaired nucleotide at the  
CC end, stability (and thus effective concentration in the cell) is improved  
CC and efficiency can be increased further by pretreating the cells with  
CC interferon. The present sequence is that of a target DNA of the invention  
XX  
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match 99.0%; Score 577.2; DB 6; Length 582;  
Best Local Similarity 99.5%; Pred. No. 2.8e-134;  
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCGAGCTGCGCCCGAGACACACGCGCTCTGTGGCAGACTTTGTAGTTAT 60  
Db 1 ATGGCGACCCCGAGCTGCGCCCGAGACACACGCGCTCTGTGGCAGACTTTGTAGTTAT 60  
QY 61 AAGCTGAGCAGAGAGGTTATGTCTGTGAGAGCTGCGCCCGGGGAGGGCCGAGAGCTGAC 120  
Db 61 AAGCTGAGCAGAGAGGTTATGTCTGTGAGAGCTGCGCCCGGGGAGGGCCGAGAGCTGAC 120  
QY 121 CCGCTGACACCAAGCCATGCGGCGAGCTGAGATGAGTTGAGACCCGCTTCCGGCGAC 180  
Db 121 CCGCTGACACCAAGCCATGCGGCGAGCTGAGATGAGTTGAGACCCGCTTCCGGCGAC 180  
QY 181 TTCTCTGATCTGGCGGCTCAGCTGATGAGTCAACAGAGATGAGACCCGCTTCCGGCGAC 180  
Db 181 TTCTCTGATCTGGCGGCTCAGCTGATGAGTCAACAGAGATGAGACCCGCTTCCGGCGAC 180  
QY 241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCACTGGGGCCGCTTGTAGCTTCTTT 300  
Db 241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCACTGGGGCCGCTTGTAGCTTCTTT 300  
QY 301 CTCTTTGGGGCTGACCTGTGTCTGAGAGTGTCAACAAGAGATGAGACCCGCTTGTAG 360  
Db 301 CTCTTTGGGGCTGACCTGTGTCTGAGAGTGTCAACAAGAGATGAGACCCGCTTGTAG 360  
QY 361 CAAGTGACAGAGTGTGTGTGCTGAGAGACGCGCTGCTGAGTATCCACAGC 420  
Db 361 CAAGTGACAGAGTGTGTGTGCTGAGAGACGCGCTGCTGAGTATCCACAGC 420  
QY 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGAGCGGGCCCTGAGAGAGCGCGG 480  
Db 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGAGCGGGCCCTGAGAGAGCGCGG 480  
QY 481 CGTCTGCGGAGGGGAGTGGCATCAGTGAGAGCAGTGTGACGGGGCCGCTGAGAG 540  
Db 481 CGTCTGCGGAGGGGAGTGGCATCAGTGAGAGCAGTGTGACGGGGCCGCTGAGAG 540  
QY 541 GGGGCGCTGTAAGTGTAGGGGCTTTTGTGTAAGAGTGA 582  
Db 541 GGGGCGCTGTAAGTGTAGGGGCTTTTGTGTAAGAGTGA 582

RESULT 5  
ABX09972  
ID ABX09972 standard; DNA; 582 BP.  
XX  
AC ABX09972;  
XX  
DT 23-JAN-2003 (first entry)  
XX  
DE Human bcl-w DNA fragment SEQ ID 37.  
XX  
KW Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;  
XX prion; inhibition; human; ds.

OS Homo sapiens.  
XX  
PN DE10100587-C1.  
XX  
PD 21-NOV-2002.  
XX  
PF 09-JAN-2001; 2001DE-01000587.  
XX  
PR 09-JAN-2001; 2001DE-01000587.  
XX  
PA (RIBO-) RIBOPHARMA AG.  
XX  
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;  
XX WPL; 2002-742209/81.  
XX

Inhibiting expression of target genes, e.g. oncogenes, in cells, by  
PT introduction of complementary double-stranded oligoribonucleotide, after  
PT treating the cell with interferon.

Disclosure; Page 35-36; 98pp; German.

CC This invention describes a novel method for inhibiting expression of a  
CC target gene by introducing into the cell that contains the target gene at  
CC least one oligoribonucleotide (dsRNA) that has a double-stranded (ds)  
CC structure of not more than 49 consecutive nucleotides (nt), where at  
CC least a segment of one strand of the ds structure is complementary with  
CC the target gene and the cells are treated with interferon before  
CC introduction of dsRNA. The method is used to inhibit expression of  
CC target genes, particularly oncogenes, cytokine genes, Id (not defined)  
CC protein genes, developmental or prion genes, or genes expressed in  
CC pathogenic organisms (particularly plasmidia) or in viruses or viroids  
CC (pathogenic in humans, animals or plants). Treating the cells with  
CC interferon greatly increases the extent to which dsRNA can inhibit  
CC expression of the target genes, and the effect is even greater when dsRNA  
CC are modified to increase their stability. ABX0936-ABX10075 represent  
CC gene fragments used to illustrate the method of the invention  
XX  
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match 99.0%; Score 577.2; DB 6; Length 582;  
Best Local Similarity 99.5%; Pred. No. 2.8e-134;  
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCGAGCTGCGCCCGAGACACACGCGCTCTGTGGCAGACTTTGTAGTTAT 60  
Db 1 ATGGCGACCCCGAGCTGCGCCCGAGACACACGCGCTCTGTGGCAGACTTTGTAGTTAT 60  
QY 61 AAGCTGAGCAGAGGTTATGTCTGTGAGAGCTGCGCCCGGGGAGGGCCGAGAGCTGAC 120  
Db 61 AAGCTGAGCAGAGGTTATGTCTGTGAGAGCTGCGCCCGGGGAGGGCCGAGAGCTGAC 120  
QY 121 CCGCTGACACCAAGCCATGCGGCGAGCTGAGATGAGTTGAGACCCGCTTCCGGCGAC 180  
Db 121 CCGCTGACACCAAGCCATGCGGCGAGCTGAGATGAGTTGAGACCCGCTTCCGGCGAC 180  
QY 181 TTCTCTGATCTGGCGGCTCAGCTGATGAGTCAACAGAGATGAGACCCGCTTCCGGCGAC 180  
Db 181 TTCTCTGATCTGGCGGCTCAGCTGATGAGTCAACAGAGATGAGACCCGCTTCCGGCGAC 180  
QY 241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCACTGGGGCCGCTTGTAGCTTCTTT 300  
Db 241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCACTGGGGCCGCTTGTAGCTTCTTT 300  
QY 301 CTCTTTGGGGCTGACCTGTGTCTGAGAGTGTCAACAAGAGATGAGACCCGCTTGTAG 360  
Db 301 CTCTTTGGGGCTGACCTGTGTCTGAGAGTGTCAACAAGAGATGAGACCCGCTTGTAG 360  
QY 361 CAAGTGACAGAGTGTGTGTGCTGAGAGACGCGCTGCTGAGTATCCACAGC 420  
Db 361 CAAGTGACAGAGTGTGTGTGCTGAGAGACGCGCTGCTGAGTATCCACAGC 420  
QY 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGAGCGGGCCCTGAGAGAGCGCGG 480

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Db 421 AGTGGGGCTGGCGGAGTTACAGCTCTATACGGGGACGGGGCCCTGGAGAGCGCGG 480
Qy 481 CGTCTGCGGAGGGGAAGTGGGCATCAGTGAGGACAGTGTGACGGGGCCGTGGCACTG 540
Db 481 CGTCTGCGGAGGGGAAGTGGGCATCAGTGAGGACAGTGTGACGGGGCCGTGGCACTG 540
Qy 541 GGGGCCCTGGTAAGTGTAGGGCCCTTTTGTAGCAAGTGA 582
Db 541 GGGGCCCTGGTAAGTGTAGGGCCCTTTTGTAGCAAGTGA 582

RESULT 6
ABL91694
ID ABL91694 standard; DNA; 582 BP.
XX
AC ABL91694;
XX
DT 28-MAY-2002 (first entry)
XX
DE Human polynucleotide SEQ ID NO 37.
XX
KW Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
KW Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
KW cytosstatic; virucide; protozoacide; antibacterial; ds.
XX
OS Homo sapiens.
XX
PN DE10100586-Cl.
XX
PD 11-APR-2002.
XX
PF 09-JAN-2001; 2001DE-01000586.
XX
PR 09-JAN-2001; 2001DE-01000586.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzner R, Lommer S, Rost S, Hadwiger P;
XX
DR WPI; 2002-270454/32.
XX
PT Inhibiting gene expression in cells, useful for e.g. treating tumors, by
PT introducing double-stranded complementary oligorNA having unpaired
PT terminal bases.
XX
PS Claim 13; Page 32; 104pp; German.
XX
CC The invention relates to a method for inhibiting expression of a target
CC gene (ABL91658-ABL91797) in a cell by introducing at least one
CC oligoribonucleotide that has a double-stranded structure consisting of at
CC most 49 sequential nucleotide pairs, with at least part of one strand
CC complementary with the target gene and has at least one end a single-
CC stranded segment of 1-4 nt. The method provides oligoribonucleotides for
CC antisense inhibition of gene expression useful e.g. for treating tumours
CC but the oligoribonucleotides may also be directed against genes present
CC in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans,
CC animals or plants) or against cytokine, id, developmental or prion genes.
CC The method provides more effective inhibition of gene expression than use
CC of known oligonucleotides, probably because the unpaired overhang
CC increases stability and thus intracellular concentration
XX
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match 99.0%; Score 577.2; DB 6; Length 582;
Best Local Similarity 99.5%; Pred. No. 2.8e-134;
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT 60
Db 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT 60
Qy 61 AAGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGCCCGGGAGAGGCCCAAGCAAGCTGAC 120
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Db 61 AAGCTGAGGAGAAAGGTTATGTCTGTGAGAGCTGGCCCCGGGAGAGGCCCAAGCAAGCTGAC 120
Qy 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTGAGAGACCCGCTTCCGGCGAC 180
Db 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTGAGAGACCCGCTTCCGGCGAC 180
Qy 181 TTCTGTATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGGCCAGCAACGCTTACC 240
Db 181 TTCTGTATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGGCCAGCAACGCTTACC 240
Qy 241 CAGGTCGCAAGAACTTTTCAAGGGGGCCCCAACTGGGGCCCTTGTAGCCTTCTT 300
Db 241 CAGGTCGCAAGAACTTTTCAAGGGGGCCCCAACTGGGGCCCTTGTAGCCTTCTT 300
Qy 301 CTCTTTGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGAGATGAAACCACTGTGGGA 360
Db 301 GTCTTTGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGAGATGAAACCACTGTGGGA 360
Qy 361 CAAGTCAGAGAGTGATGTGTGGCCCTACCTGGAGACGGGCTGTGACTGATCCACAGC 420
Db 361 CAAGTCAGAGAGTGATGTGTGGCCCTACCTGGAGACGGGCTGTGACTGATCCACAGC 420
Qy 421 AGTGGGGCTGGCGGAGTTCAACAGCTCTATACGGGACGGGGCCCTGGAGAGGCGCGG 480
Db 421 AGTGGGGCTGGCGGAGTTCAACAGCTCTATACGGGACGGGGCCCTGGAGAGGCGCGG 480
Qy 481 CGTCTGCGGAGGGGAAGTGGGCATCAGTGAGGACAGTGTGACGGGGCCGTGGCACTG 540
Db 481 CGTCTGCGGAGGGGAAGTGGGCATCAGTGAGGACAGTGTGACGGGGCCGTGGCACTG 540
Qy 541 GGGGCCCTGGTAAGTGTAGGGCCCTTTTGTAGCAAGTGA 582
Db 541 GGGGCCCTGGTAAGTGTAGGGCCCTTTTGTAGCAAGTGA 582
```

```
RESULT 7
ABT16642
ID ABT16642 standard; DNA; 3542 BP:
XX
AC ABT16642;
XX
DT 03-APR-2003 (first entry)
XX
DE Human bcl-2 gene SEQ ID No 4.
XX
KW Anti-tumour; DNazyme; bcl-2 gene; tumour; malignant; chemotherapy;
KW radiation therapy; catalytic domain; enzyme; human; ds.
XX
OS Homo sapiens.
XX
PN WO200299090-A1.
XX
PD 12-DEC-2002.
XX
PF 07-JUN-2002; 2002WO-AU000739.
XX
PR 07-JUN-2001; 2001AU-00005527.
XX
PA (JOHN ) JOHNSON & JOHNSON RES PTY LTD.
XX
PI Sun L, Wang L, Turner RJ, Saravolac EG, Dass CR;
XX
DR WPI; 2003-140617/13.
XX
PT Novel DNazyme useful for treating tumors, and for enhancing the
PT sensitivity of malignant or virus infected cells to therapy, comprises a
PT catalytic domain and binding domain contiguous to the catalytic domain.
XX
PS Disclosure; Page 44-45; 67pp; English.
XX
CC The invention relates to a DNazyme which specifically cleaves mRNA
transcribed from a member of the bcl-2 gene family. The DNazymes comprise
```



CC a catalytic domain, binding domains contiguous with the 5' and 3' end of  
 CC the catalytic domain, and therefore hybridise with, the two regions  
 CC immediately flanking the purine residue of the cleavage site within the  
 CC bcl-2 gene family mRNA, at which DNazyme-catalysed cleavage is desired. A  
 CC pharmaceutical composition comprising a DNazyme of the invention is  
 CC useful for treating tumours in a subject, and for enhancing the  
 CC sensitivity of malignant or virus infected cells infected cells to  
 CC therapy. The DNazymes are useful in diagnostics, therapeutics,  
 CC prophylaxis, research agents and in kits. The DNazymes are also useful  
 CC for increasing the susceptibility of tumour cells to anti-tumour  
 CC therapies such as chemotherapy and radiation therapy. This polynucleotide  
 CC sequence represents a human bcl-2 gene of the invention  
 XX

Sequence 3542 BP; 804 A; 817 C; 1030 G; 891 T; 0 U; 0 Other;

Query Match 98.6%; Score 575; DB 8; Length 3542;  
 Best Local Similarity 99.1%; Pred. No. 1.5e-133;  
 Matches 578; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGCGGCTCTGTGGCAGACTTTGTAGTTAT 60  
 Db 177 ATGGCGACCCAGCCTCGGCCCCAGACACACGCGGCTCTGTGGCAGACTTTGTAGTTAT 236  
 QY 61 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCCGGGAGAGGCCAGCAGCTGAC 120  
 Db 237 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCCGGGAGAGGCCAGCAGCTGAC 296  
 QY 121 CCGCTGACCAAGCCATGCGGCGAGCTGAGATGAGTTCGAGACCCGCTTCCGGCGCAC 180  
 Db 297 CCGCTGACCAAGCCATGCGGCGAGCTGAGATGAGTTCGAGACCCGCTTCCGGCGCAC 356  
 QY 181 TTCTGTATCTGCGGCTCAGCTGCATGTGACCCAGCGCTCAGCCAGCAACGCTTAC 240  
 Db 357 TTCTGTATCTGCGGCTCAGCTGCATGTGACCCAGCGCTCAGCCAGCAACGCTTAC 416  
 QY 241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCCAAGTGGGCGCCCTGTAGCTTCTT 300  
 Db 417 CAGGTCTCCGATGAATTTTCAAGGGGGCCCCAAGTGGGCGCCCTGTAGCTTCTT 476  
 QY 301 CTCTTGGGGCTGCACCTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 360  
 Db 477 GTCTTGGGGCTGCACCTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 536  
 QY 361 CAAGTCAGAGAGTGTGCTGCTTACCTGAGACCGCGCTGTGACTGATCCACAGC 420  
 Db 537 CAAGTCAGAGAGTGTGCTGCTTACCTGAGACCGCGCTGTGACTGATCCACAGC 596  
 QY 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATACCGGGACGGGGCCCTGAGAGAGCGCG 480  
 Db 597 AGTGGGGCTGGCGGAGTTCAAGCTCTATACCGGGACGGGGCCCTGAGAGAGCGCG 656  
 QY 481 CGTCTCGGGAGGGGAACTGGGCTCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540  
 Db 657 CGTCTCGGGAGGGGAACTGGGCTCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 716  
 QY 541 GGGGGCTGTACTGTAGGGGCTTTTGTGCTAGCAAGTGAA 583  
 Db 717 GGGGGCTGTACTGTAGGGGCTTTTGTGCTAGCAAGTGAA 759

RESULT 8

AAAX25132  
 ID AAAX25132 standard; DNA; 581 BP.

AC AAAX25132;

DT 05-JUL-1999 (first entry)

DE Human bcl-w gene.

KM Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;  
 KW animal model; ss.

XX

OS Homo sapiens.  
 XX  
 PN W09913710-A1.  
 XX  
 PD 25-MAR-1999.  
 XX  
 PF 16-SEP-1998; 98WO-AU000764.  
 XX  
 PR 16-SEP-1997; 97AU-00009228.  
 XX  
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
 XX  
 PI Cory S, Adams J, Print C, Gibson L, Koentgen F;  
 XX  
 DR WPI; 1999-243890/20.  
 DR P-PSDB; AAY05530.  
 XX  
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
 PT protein associated with Bcl-w.  
 XX  
 PS Claim 3; Page 32; 52pp; English.

The present sequence is the human bcl-w gene encoding Bcl-w protein (see  
 CC AAY05530), a pro-survival member of the Bcl-2 family which is widely  
 CC expressed and which is essential for spermatogenesis. The invention  
 CC relates generally to a method of treatment and to an animal model for the  
 CC identification of molecules and genetic sequences useful for inducing or  
 CC reducing fertility of male animals. Methods are provided for the  
 CC treatment of infertility, or for reducing fertility, by modulating  
 CC spermatogenesis. An animal model carries a mutation is at least one  
 CC allele of the human or murine bcl-w gene or in a gene associated with bcl  
 CC -w. Such animals have disorganised seminiferous tubules and are  
 CC substantially infertile, but possess no other major abnormalities as  
 CC determined by histological examination. They can be used to screen for  
 CC therapeutic molecules including genetic sequences capable of inducing,  
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which  
 CC can induce infertility  
 XX

Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 U; 0 Other;

Query Match 98.3%; Score 573; DB 2; Length 581;  
 Best Local Similarity 99.1%; Pred. No. 3.2e-133;  
 Matches 576; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGCGGCTCTGTGGCAGACTTTGTAGTTAT 60  
 Db 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGCGGCTCTGTGGCAGACTTTGTAGTTAT 60  
 QY 61 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCCGGGAGAGGCCAGCAGCTGAC 120  
 Db 61 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCCGGGAGAGGCCAGCAGCTGAC 120  
 QY 121 CCGCTGACCAAGCCATGCGGCGAGCTGAGATGAGTTCGAGACCCGCTTCCGGCGCAC 180  
 Db 121 CCGCTGACCAAGCCATGCGGCGAGCTGAGATGAGTTCGAGACCCGCTTCCGGCGCAC 180  
 QY 181 TTCTGTATCTGCGGCTCAGCTGCATGTGACCCAGCGCTCAGCCAGCAACGCTTAC 240  
 Db 181 TTCTGTATCTGCGGCTCAGCTGCATGTGACCCAGCGCTCAGCCAGCAACGCTTAC 240  
 QY 241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCCAAGTGGGCGCCCTGTAGCTTCTT 300  
 Db 241 CAGGTCTCCGATGAATTTTCAAGGGGGCCCCAAGTGGGCGCCCTGTAGCTTCTT 300  
 QY 301 CTCTTGGGGCTGCACCTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 360  
 Db 301 GTCTTGGGGCTGCACCTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 360  
 QY 361 CAAGTCAGAGAGTGTGCTTACCTGAGACCGCGCTGTGACTGATCCACAGC 420  
 Db 361 CAAGTCAGAGAGTGTGCTTACCTGAGACCGCGCTGTGACTGATCCACAGC 420  
 QY 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGGACGGGGCCCTGAGAGAGCGCGG 480

Db 421 AGTGGGGCTGGGGAGTTACAGCTTATACGGGACGGGGCCCTGTAGAGAGCGCGG 480  
Qy 481 CGTCTGCGGAGGGGAATGGGCATCAGTAGAGACAGTGTGACGGGGCCGTGGCACTG 540  
Db 481 CGTCTGCGGAGGGGAATGGGCATCAGTAGAGACAGTGTGACGGGGCCGTGGCACTG 540  
Qy 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTG 581  
Db 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTG 581  
RESULT 9  
AAV28334 AAV28334 standard; cDNA; 579 BP.  
XX ID AAV28334 standard; cDNA; 579 BP.  
XX AC AAV28334;  
XX DT 02-OCT-1998 (first entry)  
XX DE Human bcl-y gene.  
XX KW ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT CDS 1..579  
FT /\*tag= a  
FT /product= "bcl-y"  
FT /note= "No stop codon given"  
XX FT  
XX PN US5789201-A.  
XX PD 04-AUG-1998.  
XX PF 11-FEB-1997; 97US-00798897.  
XX PR 23-FEB-1996; 96US-0012201P.  
XX PA (COCE-) COCENSYS INC.  
XX PI Guastella J;  
XX DR WPI; 1998-446079/38.  
XX DR P-PSDB; AAW61392.  
XX XX  
XX PT Nucleic acids encoding B-cell lymphoma-y protein - useful for producing  
PT recombinant protein for use in treating uncontrolled cell growth e.g.  
PT cancers.  
XX PS Claim 3; Column 15/16; 27pp; English.  
XX CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2  
CC family, components in the cell death pathway. The bcl-2 family have both  
CC apoptotic activity and the apoptosis blocking activity. bcl-y falls in  
CC the apoptosis activity category. The recombinant protein may be used to  
CC prevent uncontrolled cell growth, either by its direct administration to  
CC recombinant genetic constructs to increase its expression in vivo. Also,  
CC antisense constructs can be used in disorders where prevention of cell  
CC death is desired  
XX SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 U; 0 Other;  
Qy Query Match 97.4%; Score 567.8; DB 2; Length 579;  
Best Local Similarity 98.8%; Pred. No. 6.3e-132;  
Matches 572; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 ATGGCGACCCAGCCTCGGCCAGACACACGAGCTGTGTGACAGCTTTGTAGTTAT 60  
Db 1 ATGGCGACCCAGCCTCGGCCAGACACACGAGCTGTGTGACAGCTTTGTAGTTAT 60  
Qy 61 AAGCTGAGGAGAGGGTTATGTCTGTGAGCTGGCCCGGAGAGGCCCAAGACAGCTGAC 120

Db 61 AAGCTGAGGAGAGGGTTATGTCTGTGAGCTGGCCCGGAGAGGCCCAAGACAGCTGAC 120  
Qy 121 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTCCAGAGACCCGCTTCCGGCGACC 180  
Db 121 CCACTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTCCAGAGACCCGCTTCCGGCGACC 180  
Qy 181 TTCTTGATCTGCGCGCTCAGCTGCATGTGACCCAGGCTCAGGCCCAAGCCTTACC 240  
Db 181 TTCTTGATCTGCGCGCTCAGCTGCATGTGACCCAGGCTCAGGCCCAAGCCTTACC 240  
Qy 241 CAGGCTCCGACGAATTTTCAAGGGGCCCCAACTGGGCGGCTTGTAGCCTTCTT 300  
Db 241 CAGGCTCCGATGAATTTTCAAGGGGCCCCAACTGGGCGGCTTGTAGCCTTCTT 300  
Qy 301 CTCTTGGGCTGCACATGTGTGCTGAGAGTGTCAACAAGAGATGAAACCACTGTGGGA 360  
Db 301 GTCTTGGGCTGCACATGTGTGCTGAGAGTGTCAACAAGAGATGAAACCACTGTGGGA 360  
Qy 361 CAAGTGACAGAGTGCATGTGTGCGCTTACCTGAGACGCGGCTGCTGATCCACAGC 420  
Db 361 CAAGTGACAGAGTGCATGTGTGCGCTTACCTGAGACGCGGCTGCTGATCCACAGC 420  
Qy 421 AGTGGGGCTGGGCGAGTTACAGCTCTATACGGGACGGGCGCTGAGAGAGCGCGG 480  
Db 421 AGTGGGGCTGGGCGAGTTACAGCTCTATACGGGACGGGCGCTGAGAGAGCGCGG 480  
Qy 481 CGTCTGCGGAGGGGAATGAGCATGAGTAGAGACAGTGTGACGGGGCCGTGGCACTG 540  
Db 481 CGTCTGCGGAGGGGAATGAGCATGAGTAGAGACAGTGTGACGGGGCCGTGGCACTG 540  
Qy 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAG 579  
Db 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAG 579  
RESULT 10  
AAAX15946 AAX15946 standard; cDNA; 579 BP.  
XX ID AAX15946 standard; cDNA; 579 BP.  
XX AC AAX15946;  
XX DT 20-MAY-1999 (first entry)  
XX DE cDNA encoding the human bcl-y protein.  
XX KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
KW premature cell death; cell death stimulator; prolonged cell life span;  
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite;  
KW ss.  
XX OS Homo sapiens.  
XX PN US5883229-A.  
XX PD 16-MAR-1999.  
XX PF 25-NOV-1997; 97US-00978523.  
XX PR 23-FEB-1996; 96US-0012201P.  
XX PR 11-FEB-1997; 97US-00798897.  
XX PA (COCE-) COCENSYS INC.  
XX PI Guastella J;  
XX DR WPI; 1999-214150/18.  
XX DR P-PSDB; AAW97392.



PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for  
PT modulating programmed cell death.

PS Disclosure; Col 15-16; 26pp; English.

XX  
CC The present sequence encodes human bcl-y protein (Hbcl-y). The  
CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-  
CC y are homologues of the bcl-2 protein thought to be involved in  
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y  
CC proteins may be used to treat conditions associated with a disruption of  
CC the cell death pathway. If they act as cell death inhibitors, they may be  
CC used in therapies to treat subjects suffering from: strokes, head trauma,  
CC Alzheimer's Disease, neural and muscular degenerative diseases  
CC (especially multiple sclerosis), myocardial infarction, vitally induced  
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis  
CC - conditions where cells under go premature cell death as a result of  
CC triggers which may or may not be apparent. They may also be used in this  
CC way to develop cell lines which remain viable in culture for an extended  
CC period. In contrast, if they act as cell death stimulators, Rbcl-y and  
CC Hbcl-y may be used to treat conditions associated with prolonged cell  
CC life span such as cancer (especially kaposi's sarcoma and lung cancer)  
CC and auto/hyperimmune diseases. They may also be used to cause cell death  
CC in, and hence control, parasites

XX Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 U; 0 Other;

Query Match 97.4%; Score 567.8; DB 2; Length 579;  
Best Local Similarity 98.8%; Pred. No. 6.3e-132;  
Matches 572; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCGAGCTCGGGCCAGACACACGGGCTCTGGTGACAGCTTTGTAGTTAT 60  
Db 1 ATGGCGACCCCGAGCTCGGGCCAGACACACGGGCTCTGGTGAGAGACTTTGTAGTTAT 60  
QY 61 AAGCTGAGGAGAAAGGTTATGTCTGTGAGAGCTGAGCCCGGGGAGAGGCCAGAGCTGAC 120  
Db 61 AAGCTGAGGAGAAAGGTTATGTCTGTGAGAGCTGAGCCCGGGGAGAGGCCAGAGCTGAC 120  
QY 121 CCGCTGACCAAGCCATGCGGGCAGCTTGAGATGAGATTGAGACCCGCTTCCGGCCGAC 180  
Db 121 CCACTGACCAAGCCATGCGGGCAGCTTGAGATGAGATTGAGACCCGCTTCCGGCCGAC 180  
QY 181 TTCTCTGATCTGGCGCTCAGCTGCATGTGACCCCAAGGCTCAGCCCAACAGCTTCACC 240  
Db 181 TTCTCTGATCTGGCGCTCAGCTGCATGTGACCCCAAGGCTCAGCCCAACAGCTTCACC 240  
QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGGCCCAACTGGGGCCGCTTGTAGCCTTCTT 300  
Db 241 CAGGTCTCCGATGAACCTTTTCAAGGGGGGCCCAACTGGGGCCGCTTGTAGCCTTCTT 300  
QY 301 CTCTTTGGGGCTGACCTGTGTGCTGAGAGTGTCAACAAGAGATGAACTGTTGGA 360  
Db 301 GTCTTTGGGGCTGACCTGTGTGCTGAGAGTGTCAACAAGAGATGAACTGTTGGA 360  
QY 361 CAAGTGACAGAGTGATGTTGGCTTACCTTGAGAGACGGGCTGTGCTGATCCACAGC 420  
Db 361 CAAGTGACAGAGTGATGTTGGCTTACCTTGAGAGACGGGCTGTGCTGATCCACAGC 420  
QY 421 AGTGGGGGCTGGCGGAGTTACAGAGCTTAATACGGGGACGGGGCCCTTGAGAGAGCGCG 480  
Db 421 AGTGGGGGCTGGCGGAGTTACAGAGCTTAATACGGGGACGGGGCCCTTGAGAGAGCGCG 480  
QY 481 CGTTCGCGGAGGAGAACTGGGCATCAGTAGAGACAGTGTGACGGGGCCGTGGCACTG 540  
Db 481 CGTTCGCGGAGGAGAACTGGGCATCAGTAGAGACAGTGTGACGGGGCCGTGGCACTG 540  
QY 541 GGGGCCCTGTAAGTGTAGGGGCTTTTGTGCTAGCAAG 579  
Db 541 GGGGCCCTGTAAGTGTAGGGGCTTTTGTGCTAGCAAG 579

RESULT 11  
ADBS2996

ID ADB52996 standard; DNA; 582 BP.  
XX  
AC ADB52996;  
XX  
XX 04-DEC-2003 (first entry)  
DT  
XX  
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3538.  
XX  
KW toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;  
KW toxicity marker; toxicity progression; drug screening;  
KW primary rat hepatocyte toxicity modelling; gene; ds.  
XX  
OS Rattus norvegicus.

XX WO2003065993-A2.

XX 14-AUG-2003.

XX 04-FEB-2003; 2003WO-US003482.

XX 04-FEB-2002; 2002US-0353171P.

XX 13-MAR-2002; 2002US-0363534P.

XX 08-APR-2002; 2002US-0370248P.

XX 10-APR-2002; 2002US-0371134P.

XX 10-APR-2002; 2002US-0371135P.

XX 11-APR-2002; 2002US-0371413P.

XX 19-APR-2002; 2002US-0373601P.

XX 19-APR-2002; 2002US-0373602P.

XX 22-APR-2002; 2002US-0374139P.

XX 08-MAY-2002; 2002US-0378370P.

XX 09-MAY-2002; 2002US-0378652P.

XX 09-MAY-2002; 2002US-0378653P.

XX 09-JUL-2002; 2002US-0394230P.

XX 09-JUL-2002; 2002US-0394253P.

XX 04-SEP-2002; 2002US-0407688P.

XX 28-JAN-2003; 2003US-0442900P.

(GENE-) GENE LOGIC INC.

PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;  
PI Elashoff M;

DR WPI; 2003-731472/69.

XX  
XX  
PT Determining if a compound induces a toxic effect on a tissue or cell, for  
PT identifying hepatotoxic compounds, comprises comparing a gene expression  
PT profile of a tissue or cell sample to a database of Tox mean and non-Tox  
PT mean values.

PS Claim 44; SEQ ID NO 3538; 874pp; English.

XX  
CC The present invention describes a method for determining whether a  
CC compound induces a toxic effect on a tissue or cell. The method comprises  
CC preparing a gene expression profile of a tissue or cell sample exposed to  
CC the compound, and comparing the gene expression profile to a database  
CC comprising data or information on the Tox mean and non-Tox mean value.  
CC The method is useful for predicting or identifying at least one toxic  
CC effect, particularly hepatotoxicity, of a test or unknown compound. The  
CC genes listed in the specification are useful as diagnostic or toxicity  
CC markers for the prediction or identification of the physiological state  
CC of tissue or cell sample that has been exposed to a compound, or to  
CC identify or predict the toxic effects of a compound or an agent. These  
CC may also be used as markers for monitoring toxicity progression or for  
CC drug screening. The present sequence represents a primary rat hepatocyte  
CC toxicity modelling related gene sequence from the present invention.

XX Sequence 582 BP; 111 A; 157 C; 200 G; 114 T; 0 U; 0 Other;

Query Match 90.5%; Score 527.6; DB 10; Length 582;  
Best Local Similarity 94.2%; Pred. No. 6.9e-122;  
Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGTTAT 60  
DB 1 ATGGCGACCCAGCCTCAAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
QY 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGCCCCGGGGAGGGGCCAGCAGCTGAC 120  
DB 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGCCCCGGGGAGGGGCCAGCAGCCGAC 120  
QY 121 CCGCTGACCAAGCCATGCGGCGAGCTGAGATGATTCAGACCCGCTTCGGCGCACC 180  
DB 121 CCGCTGACCAAGCCATGCGGCGAGCTGAGAGAGTTGAGACCCGCTTCGGCGCACC 180  
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
DB 181 TTCTCTGACCTGGCGGCTCAGCTACACGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
QY 241 CAGGCTCCGACGAATTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCCTTCTTT 300  
DB 241 CAGGTTCCGACGAATTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCATTCTTT 300  
QY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAACTGCTGCGA 360  
DB 301 GTCTTTGGGGCTGCTGTGTGTGCTGAGAGTGTCAACAAGAAATGAGCCATTGTGGGA 360  
QY 361 CAAGTGACAGATGATGTGCTGACCTACCTGAGACGCGGCTGTGCTGAGTCCACAGC 420  
DB 361 CAAGTGACAGATGATGTGCTGACCTACCTGAGACACGCTTGTGCTGAGTCCACAGC 420  
QY 421 AGTGGGGCTGGCGGAGTTACAGCTCTATACGGGGACGGGCGCTGAGAGAGCGCGG 480  
DB 421 AGTGGGGCTGGCGGAGTTACAGCTCTATACGGGGACGGGCGCTGAGAGAGCGCGG 480  
QY 481 CGTCTCGGAGGGGAACTGGGCATCAGTGAGAGACAGTGTGACGGGGCGCTGGCACTG 540  
DB 481 CGTCTCGGAGGGGAACTGGGCATCAGTGAGAGACAGTGTGACGGGGCGCTGTGGCACTG 540  
QY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTGA 582  
DB 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTGA 582  
RESULT 12  
AAV28333  
ID AAV28333 standard; cDNA; 579 BP.  
XX AAV28333;  
AC AAV28333;  
XX  
DT 02-OCT-1998 (first entry)  
XX  
DE Rat bcl-y gene.  
XX  
KM ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.  
OS Rattus sp.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..579  
FT /tag= a  
FT /product= "bcl-y"  
FT /note= "No stop codon given"  
XX  
PN US5789201-A.  
XX  
PD 04-AUG-1998.  
XX  
PF 11-FEB-1997; 97US-00798897.  
XX  
PR 23-FEB-1996; 96US-0012201P.  
XX  
PA (COCE-) COCENSYS INC.  
XX  
PI Guastella J;

XX  
DR WPI; 1998-446079/38.  
DR P-PSDB; AAW61391.  
XX  
PT Nucleic acids encoding B-cell lymphoma-y protein - useful for producing  
PT recombinant protein for use in treating uncontrolled cell growth e.g.  
PT cancers.  
XX  
PS Claim 2; Column 13/14; 27pp; English.  
XX  
CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2  
CC family, components in the cell death pathway. The bcl-2 family have both  
CC apoptotic activity and the apoptosis blocking activity. bcl-y falls in  
CC the apoptosis activity category. The recombinant protein may be used to  
CC prevent uncontrolled cell growth, either by its direct administration to  
CC recombinant genetic constructs to increase its expression in vivo. Also,  
CC antisense constructs can be used in disorders where prevention of cell  
CC death is desired  
XX  
SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;  
Query Match 89.7%; Score 523; DB 2; Length 579;  
Best Local Similarity 94.0%; Pred. No. 9.6e-121;  
Matches 544; Conservative 0; Mismatches 35; Indels 0; Gaps 0;  
QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGTTAT 60  
DB 1 ATGGCGACCCAGCCTCAAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
QY 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGCCCCGGGGAGGGGCCAGCAGCTGAC 120  
DB 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGCCCCGGGGAGGGGCCAGCAGCCGAC 120  
QY 121 CCGCTGACCAAGCCATGCGGCGAGCTGAGATGATTCAGACCCGCTTCGGCGCACC 180  
DB 121 CCGCTGACCAAGCCATGCGGCGAGCTGAGAGAGTTGAGAACCCGCTTCGGCGCACC 180  
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
DB 181 TTCTCTGACCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
QY 241 CAGGCTCCGACGAATTTTCAAGGGGGCCCAACTGGGGCGCTTGTAGCCTTCTTT 300  
DB 241 CAGGTTCCGACGAATTTTCAAGGGGGCCCAACTGGGGCGCTTGTAGCATTCTTT 300  
QY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAACTGCTGCGA 360  
DB 301 GTCTTTGGGGCTGCCCTGTGTGTGCTGAGAGTGTCAACAAGAAATGAGCCATTGTGGGA 360  
QY 361 CAAGTGACAGATGATGTGCTGACCTACCTGAGACGCGGCTGTGCTGAGTCCACAGC 420  
DB 361 CAAGTGACAGATGATGTGCTGACCTACCTGAGACACGCTTGGCTGACTGATCCACAGC 420  
QY 421 AGTGGGGCTGGCGGAGTTACAGCTCTATACGGGGACGGGCGCTGAGAGAGCGCGG 480  
DB 421 AGTGGGGCTGGCGGAGTTACAGCTCTATACGGGGACGGGCGCTGAGAGAGCGCGG 480  
QY 481 CGTCTCGGAGGGGAACTGGGCATCAGTGAGAGACAGTGTGACGGGGCGCTGGCACTG 540  
DB 481 CGTCTCGGAGGGGAACTGGGCATCAGTGAGAGACAGTGTGACGGGGCGCTGTGGCACTG 540  
QY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGCTAGCAAG 579  
DB 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGCTAGCAAG 579  
RESULT 13  
AAK15945  
ID AAK15945 standard; cDNA; 579 BP.  
XX AAK15945;  
AC AAK15945;  
XX  
DT 20-MAY-1999 (first entry)

Page

DB 181 TTCTCTGACTGGCCGCTCAGCTACACGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240

QY 241 CAGGTCCTCCGACGAACTTTTCAAGGGGGCCCCCACTGGGGCCGCTTGTAGCTTCTTT 300

DB 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCCCACTGGGGCCGCTTGTAGCTTCTTT 300

QY 301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGAGATGGAACCACTGGTGGGA 360

DB 361 CAAGTGCAAGAGTGTGATGTGGCTTACCTGAGACCGCGGCTGTGCACTGATCCACAGC 420

QY 421 AGTGGGGCTGGCGCGAGTTCAAGCTCTATACGGGAGCGGGCCCTTGAGAGAGCGCGG 480

DB 481 CGTCTGCGGAGAGGGGAACTGGGCATCAGTGAAGACAGAGTGTGACCGGGCCCTTGAGAGAGCGCGG 480

QY 481 CGTCTGCGGAGAGGGGAACTGGGCATCAGTGAAGACAGAGTGTGACCGGGCCCTTGAGAGAGCGCGG 480

DB 541 GGGGGCCCTGTGTAAGTGTGAGGGCCCTTTTGTAGCAAG 579

541 GGGGGCCCTGTGTAAGTGTGAGGGCCCTTTTGTAGCAAG 579

RESULT 14

ID AAX25133 standard; DNA; 581 BP.

AC AAX25133;

XX 05-JUL-1999 (first entry)

DT Mouse bcl-w gene.

DE Mouse bcl-w gene.

XX KW Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;

OS animal model; ss.

XX Mus sp.

PN W09913710-A1.

PD 25-MAR-1999.

XX 16-SEP-1998; 98WO-AU000764.

PF 16-SEP-1997; 97AU-00009228.

PR (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX WPI; 1999-243890/20.

XX P-PSDB; AAY05531.

PT An animal model exhibiting reduced levels of a Bcl-w protein and/or

PT protein associated with Bcl-w.

XX Claim 3; Page 34; 52pp; English.

XX The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see

CC expressed and which is essential for spermatogenesis. The invention

CC relates generally to a method of treatment and to an animal model

CC identification of molecules and genetic sequences useful for the

CC treatment of infertility, or for reduction of fertility for the

CC spermatogenesis. An animal model exhibiting reduced levels of a Bcl-w

CC allele of the bcl-w gene, or for reduction of fertility for the



CC substantially infertile, but possess no other major abnormalities as  
CC determined by histological examination. They can be used to screen for  
CC therapeutic molecules including genetic sequences capable of inducing,  
CC enhancing or otherwise facilitating spermatogenesis in animals, or which  
CC can induce infertility

XX Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 U; 0 Other;

Query Match 89.5%; Score 521.8; DB 2; Length 581;  
Best Local Similarity 93.6%; Pred. No. 1.9e-120;  
Matches 544; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

OY 1 ATGGCGACCCCAAGCCTCGGCCAGACACACGGGCTCTGGTGACAGCTTTGTAGTTAT 60  
DB 1 ATGGCGACCCCAAGCCTCAACCCAGACACACGGGCTCTAGTGCTGACTTTGTAGGCTAT 60  
OY 61 AAGCTGAGGCAAGGGTTATGTCTGTGAGCTGGCCCCGGGAGGGGCCAGAGCTGAC 120  
DB 61 AAGCTGAGGCAAGGGTTATGTCTGTGAGCTGGCCCCGGGAGGGGCCAGCGCCGAC 120  
OY 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGAGTTCGAGACCCGCTCCGGCGCAC 180  
DB 121 CCGCTGACCAAGCCATGCGGGCTGCTGAGACGAGTTGAGACCCGTTCCGGCCGACC 180  
OY 181 TTCTCTGATCTGCGCGCTCAGCTGCATGTGACCCCAAGGCTCAGCCCAAGCAAGCTTACC 240  
DB 181 TTCTCTGATCTGCGCGCTCAGCTGCATGCATGACGCTCAAGGCTCAGCCCAAGCAAGCTTACC 240  
OY 241 CAGGCTCCGACGAATTTTCAAGGGGGCCCCCACTGGGGCCGCTTGAGCTTCTTT 300  
DB 241 CAGGTTCCGACGAATTTTCAAGGGGGCCCCCACTGAGGGCCGCTTGAGCTTCTTT 300  
OY 301 CTCTTTGGGCTGCACTGTGTGTGAGAGTGTCAACAAGAGATGGAACAAGCTGTGGA 360  
DB 301 GTCTTTGGGCTGCTGCTGTGTGTGAGAGTGTCAACAAGAAATGAGCTTTGTGGA 360  
OY 361 CAAGTGACAGATGATGTGCTTACCTGAGACGCGGCTGTGCTGATCCACAGC 420  
DB 361 CAAGTGACAGATGATGTGCTTACCTGAGACAGCTGTGCTGATCCACAGC 420  
OY 421 AGTGGGGCTGGCGGAGTTTCAAGCTCTATACGGGGACGGGCCCTGAGGAGGCGCG 480  
DB 421 AGTGGGGCTGGCGGAGTTTCAAGCTCTATACGGGGACGGGCCCTGAGGAGGCGCG 480  
OY 481 CGTCTCGGGAGGGGAATGCGCATCAGTGAGAGACAGTGCTGACGGGGCCGTGGCACTG 540  
DB 481 CGTCTCGGGAGGGGAATGCGCATCAGTGAGAGACAGTGCTGACGGGGCCGTGGCACTG 540  
OY 541 GGGGCCCTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTG 581  
DB 541 GGGGCCCTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTG 581

RESULT 15  
AAT96578  
ID AAT96578 standard; DNA; 581 BP.

XX AAT96578;  
AC AAT96578;  
DT 22-APR-1998 (first entry)  
XX Mouse bcl-w DNA.  
DE Mouse bcl-w DNA.  
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
KM diagnosis; degenerative disease; ss.  
XX  
OS Mus sp.

XX Key Location/Qualifiers  
FH 1.507  
FT /\*tag= a  
FT /product= "bcl-w"  
FT /note= "q"

XX PN MO9735971-A1.  
XX 02-OCT-1997.  
XX 27-MAR-1997; 97WO-AU000199.  
XX 27-MAR-1996; 96AU-00008965.  
XX (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX Cory S, Adams JM, Gibson LM, Holmgren SP;  
XX WPI; 1997-489635/45.  
XX P-PSDB; AAW36048.  
XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce or  
PT inhibit cell survival, e.g. for treatment of cancer and degenerative  
PT diseases.  
XX  
PS Claim 3; Page 50-51; 86pp; English.

CC This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene  
CC family. This gene promotes cell survival, so its modulation is useful in  
CC treatment of cancer or auto-immune diseases, degenerative diseases (e.g.  
CC stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,  
CC hypoxia, ischaemia, human immunodeficiency virus infection or in cell  
CC transplants. Up-regulation of the gene can also be used to modify cell  
CC lines cultured in vivo, e.g. to develop new lines, to facilitate  
CC isolation of hybridomas and to increase survival of primary explants  
CC during genetic modification. It can be used to produce recombinant Bcl-w  
CC for therapy, diagnosis, antibody production or screening of potential  
CC modulators

XX SQ Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 U; 0 Other;  
Query Match 85.9%; Score 501; DB 2; Length 581;  
Best Local Similarity 91.4%; Pred. No. 3e-115;  
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

OY 1 ATGGGACCCCAAGCCTCGGCCAGACACAGGGCTCTGGTGACAGCTTTGTAGTTAT 60  
DB 1 ATGGGACCCCAAGCCTCAACCCAGACACAGCGCTCTAGTGCTGACTTTGTAGGCTAT 60  
OY 61 AAGTGAGCAGAAAGGTTATGTGTGTGAGAGCTGGCCCCGGGAGGGCCCCAGAGCTGAC 120  
DB 61 AAGTGAGCAGAAAGGTTATGTGTGTGAGAGCTGGCCCCGGGAGGGCCCCAGAGCTGAC 120  
OY 121 CCGTGACCAAGCCATGCGGGCAGCTGAGATGAGTTCGAGACCCGCTTCCGGCGCAC 180  
DB 121 CCGTGACCAAGCCATGCGGGCTGTGTGAGAGAGAGTTGAGACCCGTTCCGGCGCAC 180  
OY 181 TTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAAGGCTCAGCCCAAGCAAGCTTACC 240  
DB 181 TTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAAGGCTCAGCCCAAGCAAGCTTACC 240  
OY 241 CAGGTTCCGACGAATTTTCAAGGGGGCCCCCACTGGGGCCGCTTGTGCAATCTTT 300  
DB 241 CAGGTTCCGACGAATTTTCAAGGGGGCCCCCACTAGGGGCGCTTGTGCAATCTTT 300  
OY 301 CTCTTTGGGCTGCACTGTGTGTGAGAGTGTCAACAAGAGATGGAACAAGCTGTGGA 360  
DB 301 GTCTTTGGGCTGCCCTGTGTGTGAGAGTGTCAACAAGAAATGAGCCCTTGTGGA 360  
OY 361 CAAGTGACAGATGATGTGCTTACCTGAGACGCGGCTGTGCTGATCCACAGC 420  
DB 361 CAAGTGACAGATGATGTGCTTACCTGAGACAGCTGTGCTGATCCACAGC 420  
OY 421 AGTGGGGCTGGCGGAGTTTCAAGCTCTATACGGGACGGGCCCTGAGAGGCGCGG 480  
DB 421 AGTGGGGCTGGCGGAGTTTCAAGCTCTATACGGGACGGGCCCTGAGAGGCGCACG 480  
OY 481 CGTCTCGGGAGGGGAATGAGATCAGTGAGAGACAGTGCTGACGGGGCCGTGGCACTG 540

Db 481 CGTCTGCGGAGGCAACTGGGCATGAGTGCACAGTGTGACGGGGCGTGGCACTG 540  
QY 541 GGGGCCCTGGTAAGTGTAGGGCCCTTTTGTAGCAAGTG 581  
Db 541 GGGGCCCTGGTAAGTGTAGGGCCCTTTTGTAGCAAGTG 581

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Total number of hits satisfying chosen parameters: 2405568

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Maximum Match 100%  
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2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/PCTUS.COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	583	100.0	583	4	US-09-155-327G-6
2	572.4	98.2	582	4	US-09-949-016-5057
3	567.8	97.4	579	1	US-08-798-897-2
4	567.8	97.4	579	2	US-08-978-523-2
5	523	89.7	579	1	US-08-798-897-1
6	523	89.7	579	2	US-08-978-523-1
7	501	85.9	581	4	US-09-155-327G-8
8	424	72.7	1098	4	US-09-010-147B-23
9	423.6	72.7	1864	3	US-09-149-476-130
10	423.4	72.6	5199	4	US-09-949-016-16799
11	414.6	71.1	601	4	US-09-949-016-177003
12	131	22.5	926	1	US-08-081-448-5
13	131	22.5	926	2	US-08-470-670A-6
14	131	22.5	926	3	US-08-481-739-1
15	131	22.5	926	3	US-09-167-921-1
16	131	22.5	926	3	US-09-277-020-39
17	131	22.5	926	3	US-09-323-743-1
18	131	22.5	926	3	US-08-461-511A-6
19	131	22.5	926	3	US-09-271-014A-5
20	131	22.5	926	4	US-09-023-655-1430
21	131	22.5	926	4	US-09-814-915A-106
22	131	22.5	926	5	PCT-US94-07089-6
23	131	22.5	1236	4	US-09-639-245-1
24	127.6	21.9	1455	4	US-09-639-245-7
25	125	21.4	711	4	US-09-741-238-1
26	123.4	21.2	717	2	US-08-465-485A-20
27	123.4	21.2	717	3	US-09-080-285-20

28	123.4	21.2	4825	6	5459251-1	Patent No. 5459251
29	123.4	21.2	4825	6	5459251-1	Patent No. 5459251
30	123.4	21.2	5086	2	US-08-465-485A-19	Sequence 19, Appl
31	123.4	21.2	5086	2	US-08-365-486A-14	Sequence 14, Appl
32	123.4	21.2	5086	3	US-09-080-285-19	Sequence 19, Appl
33	123.4	21.2	5086	3	US-08-880-342-14	Sequence 14, Appl
34	123.4	21.2	5086	3	US-09-724-426-19	Sequence 19, Appl
35	123.4	21.2	5086	3	US-09-233-527-7	Sequence 7, Appl
36	123.4	21.2	5086	5	PCT-US93-05651-4	Sequence 4, Appl
37	123.4	21.2	5086	5	PCT-US93-06251-2	Sequence 2, Appl
38	123.4	21.2	5094	3	US-09-234-186-7	Sequence 7, Appl
39	123.4	21.2	5104	6	5506344-1	Patent No. 5506344
40	123.4	21.2	5104	6	5506344-1	Patent No. 5506344
41	123.2	21.1	60489	4	US-09-949-016-16287	Sequence 16287, A
42	121.8	20.9	760	1	US-08-405-702A-11	Sequence 11, Appl
43	121.8	20.9	6030	4	US-09-023-655-1015	Sequence 1015, Ap
44	120.4	20.7	1384	4	US-08-839-367-1	Sequence 1, Appl
45	120.2	20.6	1846	2	US-08-365-486A-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-09-155-327G-6  
; Sequence 6, Application US/09155327G  
; Patent No. 6790637  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2  
; FILE REFERENCE: 2096584  
; CURRENT APPLICATION NUMBER: US/09/155,327G  
; PRIOR FILING DATE: 1999-03-29  
; PRIOR APPLICATION NUMBER: PN8965  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 583  
; TYPE: DNA  
; ORGANISM: HUMAN  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(579)  
US-09-155-327G-6

Query Match	100.0%;	Score 583;	DB 4;	Length 583;
Best Local Similarity	100.0%;	Pred. No. 1.7e-144;		
Matches	583;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;
QY	1	ATGGCGACCCAGCCTCGGCCAGACACACGCGGCTCTGTGGCAGACTTGTAGTTAT	60	
DB	1	ATGGCGACCCAGCCTCGGCCAGACACACGCGGCTCTGTGGCAGACTTGTAGTTAT	60	
QY	61	AAGCTGAGGAGAGGGTTATGTCTGTGAGCTGGCCCCGGGAGGAGGCCAGAGCTGAC	120	
DB	61	AAGCTGAGGAGAGGGTTATGTCTGTGAGCTGGCCCCGGGAGGAGGCCAGAGCTGAC	120	
QY	121	CCGCTGACCAAGCCATGCGGCGAGCTGAGATGATTGAGACCCGCTTCGGCGCACC	180	
DB	121	CCGCTGACCAAGCCATGCGGCGAGCTGAGATGATTGAGACCCGCTTCGGCGCACC	180	
QY	181	TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCAAC	240	
DB	181	TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCAAC	240	
QY	241	CAGGTCTCCAGCAACTTTTCAAGGGGGCCCACTGGGGCGGCTTGTAGCTTCTTT	300	
DB	241	CAGGTCTCCAGCAACTTTTCAAGGGGGCCCACTGGGGCGGCTTGTAGCTTCTTT	300	
QY	301	CTCTTTGGGGCTGCACTGTGTGCTGAGTGTCAACAGAGATGGAACCACTGTGGGA	360	
DB	301	CTCTTTGGGGCTGCACTGTGTGCTGAGTGTCAACAGAGATGGAACCACTGTGGGA	360	

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Db      301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 360
QY      361 CAAGTCAGAGAGTGAATGGTGGCCCTACCTGGAGACGGCGCTGTGACTGTGATCCACAGC 420
Db      361 CAAGTCAGAGAGTGAATGGTGGCCCTACCTGGAGACGGCGCTGTGACTGTGATCCACAGC 420
QY      421 AGTGGGGCTGGCGGAGTTTCAACAGCTCTATAACGGGACGGGGCCCTGGAGAGCGCGG 480
Db      421 AGTGGGGCTGGCGGAGTTTCAACAGCTCTATAACGGGACGGGGCCCTGGAGAGCGCGG 480
QY      481 CGTCTCGGAGAGGGAACTGGGCATCACTGAGAGACAGTGTGACGGGGCCCTGGCACTG 540
Db      481 CGTCTCGGAGAGGGAACTGGGCATCACTGAGAGACAGTGTGACGGGGCCCTGGCACTG 540
QY      541 GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAGTGAA 583
Db      541 GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAGTGAA 583
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## RESULT 2

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US-09-949-016-5057
; Sequence 5057, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5057
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5057
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Query Match      98.2%; Score 572.4; DB 4; Length 582;
Best Local Similarity 99.0%; Pred. No. 1.1e-141;
Matches 576; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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QY      1 ATGGCGACCCCGACCTCGGCCCCAGACACACACGGGCTGTGTGGCAGACTTTAGATTAT 60
Db      1 ATGGCGACCCCGACCTCGGCCCCAGACACACACGGGCTGTGTGGCAGACTTTAGATTAT 60
QY      61 AAGCTGAGGAGAGGGTTATGTCTGTGAGCTGGCCCCGGGAGGGCCCCAGCAGCTGAC 120
Db      61 AAGCTGAGGAGAGGGTTATGTCTGTGAGCTGGCCCCGGGAGGGCCCCAGCAGCTGAC 120
QY      121 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCCGGCGCAC 180
Db      121 CCACTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCCGGCGCAC 180
QY      181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCCAACAGCTTCAAC 240
Db      181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCCAACAGCTTCAAC 240
QY      241 CAGTCTCCGACGAATTTTCAAGGGGGCCCCCAACTGGGGCCGCTTGTAGCTTCTTT 300
Db      241 CAGTCTCCGACGAATTTTCAAGGGGGCCCCCAACTGGGGCCGCTTGTAGCTTCTTT 300
QY      301 CTCTTTGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 360
Db      301 GTCTTTGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 360
QY      361 CAAGTCAGAGAGTGAATGGTGGCCCTACCTGGAGACGGCGCTGTGACTGTGATCCACAGC 420
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Db      361 CAAGTCAGAGAGTGAATGGTGGCCCTACCTGGAGACGGCGCTGTGACTGTGATCCACAGC 420
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Db      421 AGTGGGGCTGGCGGAGTTTCAACAGCTCTATAACGGGACGGGGCCCTGGAGAGCGCGG 480
QY      481 CGTCTCGGAGAGGGAACTGGGCATCACTGAGAGACAGTGTGACGGGGCCCTGGCACTG 540
Db      481 CGTCTCGGAGAGGGAACTGGGCATCACTGAGAGACAGTGTGACGGGGCCCTGGCACTG 540
QY      541 GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAGTGAA 582
Db      541 GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAGTGAA 582
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## RESULT 3

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US-08-798-897-2
; Sequence 2, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-08-798-897-2
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Query Match      97.4%; Score 567.8; DB 1; Length 579;
Best Local Similarity 98.8%; Pred. No. 1.8e-140;
Matches 572; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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QY      1 ATGGCGACCCCGACCTCGGCCCCAGACACACGGGCTGTGTGGCAGACTTTAGATTAT 60
Db      1 ATGGCGACCCCGACCTCGGCCCCAGACACACGGGCTGTGTGGCAGACTTTAGATTAT 60
QY      61 AAGCTGAGGAGAGGGTTATGTCTGTGAGAGCTGGCCCCGGGAGGGCCCCAGCAGCTGAC 120
Db      61 AAGCTGAGGAGAGGGTTATGTCTGTGAGAGCTGGCCCCGGGAGGGCCCCAGCAGCTGAC 120
QY      121 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCCGGCGCAC 180
Db      121 CCACTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCCGGCGCAC 180
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OY 241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCCCACTGGGGCCGCTTGTAGCCTTCTTT 300
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OY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 360
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Db 301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 360
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Db 361 CAAGTGCAGAGTGTGATGGTGGCTTACCTGAGACGCGGCTGTGACTGTGATCCACAGC 420
OY 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGAGACGGGGCCCTGAGAGAGCGCGG 480
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Db 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGAGACGGGGCCCTGAGAGAGCGCGG 480
OY 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540
    |||||||
Db 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540
OY 541 GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAG 579
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Db 541 GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAG 579
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## RESULT 4

US-08-978-523-2  
; Sequence 2, Application US/08978523  
; Patent No. 5883229

## GENERAL INFORMATION:

APPLICANT: Guastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
TITLE OF INVENTION: Homologue

NUMBER OF SEQUENCES: 53

## CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,523

FILING DATE: herewith

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/798,897

FILING DATE: February 11, 1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1483.0140002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 579 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cDNA

US-08-978-523-2

Query Match 97.4%; Score 567.8; DB 2; Length 579;  
Best Local Similarity 98.8%; Pred. No. 1.8e-140;  
Matches 572; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
OY 1 ATGGCGACCCCAAGCTTCGGCCCCAGACACAGGGGCTGTGGTGGACACTTTGTAGTTAT 60
    |||||||
Db 1 ATGGCGACCCCAAGCTTCGGCCCCAGACACAGGGGCTGTGGTGGACACTTTGTAGTTAT 60
OY 61 AAGCTGAGGCAAGAGGTTATGTCTGTGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 120
    |||||||
Db 61 AAGCTGAGGCAAGAGGTTATGTCTGTGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 120
OY 121 CCGCTGACCAAGCCATGCGGCGAGCTGAGATGATTGAGACCCGCTTCCGGCGCAC 180
    |||||||
Db 121 CCACTGACCAAGCCATGCGGCGAGCTGAGATGATTGAGACCCGCTTCCGGCGCAC 180
OY 181 TTCTGTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240
    |||||||
Db 181 TTCTGTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240
OY 241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCCCACTGGGGCCGCTTGTAGCCTTCTTT 300
    |||||||
Db 241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCCCACTGGGGCCGCTTGTAGCCTTCTTT 300
OY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 360
    |||||||
Db 301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 360
OY 361 CAAGTGCAGAGTGTGATGGTGGCTTACCTGAGACGCGGCTGTGACTGTGATCCACAGC 420
    |||||||
Db 361 CAAGTGCAGAGTGTGATGGTGGCTTACCTGAGACGCGGCTGTGACTGTGATCCACAGC 420
OY 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGAGACGGGGCCCTGAGAGAGCGCGG 480
    |||||||
Db 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGAGACGGGGCCCTGAGAGAGCGCGG 480
OY 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540
    |||||||
Db 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540
OY 541 GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAG 579
    |||||||
Db 541 GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAG 579
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## RESULT 5

US-08-798-897-1  
; Sequence 1, Application US/08798897  
; Patent No. 5789201

## GENERAL INFORMATION:

APPLICANT: Guastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
TITLE OF INVENTION: Homologue

NUMBER OF SEQUENCES: 53

## CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/798,897

FILING DATE: February 11, 1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 579 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
US-08-798-897-1

Query Match 89.7%; Score 523; DB 1; Length 579;  
Best Local Similarity 94.0%; Pred. No. 1.2e-128;  
Matches 544; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCGGCCCCCAGACACACCGGGCTTGTGGCAGACTTGTAGTTAT 60  
Db 1 ATGGCGACCCAGCCTCAACCCAGACACACCGGGCTTGTAGTGTAGTGTAT 60  
QY 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGAGCTGGCCCCGGGAGGGCCAGCAGTAC 120  
Db 61 AAGCTGAGACAGAAAGGTTATGTCTGTGAGAGCTGGCCCCGGGAGGGCCAGCAGTAC 120  
QY 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATAGTTGAGACCCGCTTCCGGCGAC 180  
Db 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATAGTTGAGACCCGCTTCCGGCGAC 180  
QY 181 TTCTGTATCTGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCA 240  
Db 181 TTCTGTATCTGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCA 240  
QY 241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCCAAGTGGGGCCGCTTGTAGCTTCTT 300  
Db 241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCCAAGTGGGGCCGCTTGTAGCTTCTT 300  
QY 301 CTCTTTGGGCTGCACTGTGTGCTGAGATGTCAACAAGAGATGAAACCACTGTGGGA 360  
Db 301 GTCTTTGGGCTGCGCTGTGTGCTGAGATGTCAACAAGAGATGAAACCACTGTGGGA 360  
QY 361 CAAGTGACAGATGATGTGCTGAGATGTGAGACCGGGCTGTGACTGATCCACAGC 420  
Db 361 CAAGTGACAGATGATGTGCTGAGATGTGAGACCGGGCTGTGACTGATCCACAGC 420  
QY 421 AGTGGGGCTGGGCGAGTTCAAGCTCTATACGGGGACGGGGCCCTGAGAGAGCGCG 480  
Db 421 AGTGGGGCTGGGCGAGTTCAAGCTCTATACGGGGACGGGGCCCTGAGAGAGCGCG 480  
QY 481 CGTTCGGGAGAGGGAATGCGCATCAGTGAGAGAGTGTGACGGGGCCGTGACATG 540  
Db 481 CGTTCGGGAGAGGGAATGCGCATCAGTGAGAGAGTGTGACGGGGCCGTGACATG 540  
QY 541 GGGGCCCTGTACTGTAGGGGCTTTTGTGTAACAAG 579  
Db 541 GGGGCCCTGTACTGTAGGGGCTTTTGTGTAACAAG 579

RESULT 6  
US-08-978-523-1

Sequence 1, Application US/08978523  
Patent No. 5883229  
GENERAL INFORMATION:  
APPLICANT: Guastella, John  
TITLE OF INVENTION: Genes Coding for Bcl-y, a Bcl-2  
TITLE OF INVENTION: Homologue  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC

COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,523  
FILING DATE: herewith  
CLASSIFICATION: 424  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 579 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
US-08-978-523-1

Query Match 89.7%; Score 523; DB 2; Length 579;  
Best Local Similarity 94.0%; Pred. No. 1.2e-128;  
Matches 544; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCGGCCCCCAGACACACCGGGCTTGTGGCAGACTTGTAGTTAT 60  
Db 1 ATGGCGACCCAGCCTCAACCCAGACACACCGGGCTTGTAGTGTAGTGTAT 60  
QY 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGAGCTGGCCCCGGGAGGGCCAGCAGTAC 120  
Db 61 AAGCTGAGACAGAAAGGTTATGTCTGTGAGAGCTGGCCCCGGGAGGGCCAGCAGTAC 120  
QY 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATAGTTGAGACCCGCTTCCGGCGAC 180  
Db 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATAGTTGAGACCCGCTTCCGGCGAC 180  
QY 181 TTCTGTATCTGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCA 240  
Db 181 TTCTGTATCTGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCA 240  
QY 241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCCAAGTGGGGCCGCTTGTAGCTTCTT 300  
Db 241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCCAAGTGGGGCCGCTTGTAGCTTCTT 300  
QY 301 CTCTTTGGGCTGCACTGTGTGCTGAGATGTCAACAAGAGATGAAACCACTGTGGGA 360  
Db 301 GTCTTTGGGCTGCGCTGTGTGCTGAGATGTCAACAAGAGATGAAACCACTGTGGGA 360  
QY 361 CAAGTGACAGATGATGTGCTGAGATGTGAGACCGGGCTGTGACTGATCCACAGC 420  
Db 361 CAAGTGACAGATGATGTGCTGAGATGTGAGACCGGGCTGTGACTGATCCACAGC 420  
QY 421 AGTGGGGCTGGGCGAGTTCAAGCTCTATACGGGGACGGGGCCCTGAGAGAGCGCG 480  
Db 421 AGTGGGGCTGGGCGAGTTCAAGCTCTATACGGGGACGGGGCCCTGAGAGAGCGCG 480  
QY 481 CGTTCGGGAGAGGGAATGCGCATCAGTGAGAGAGTGTGACGGGGCCGTGACATG 540  
Db 481 CGTTCGGGAGAGGGAATGCGCATCAGTGAGAGAGTGTGACGGGGCCGTGACATG 540  
QY 541 GGGGCCCTGTACTGTAGGGGCTTTTGTGTAACAAG 579  
Db 541 GGGGCCCTGTACTGTAGGGGCTTTTGTGTAACAAG 579



Db 541 GGGGCCCTGTAACTGTAGGGCCCTTTTGTAGCAAG 579

RESULT 7

US-09-155-327G-8  
 ; Sequence 8, Application US/09155327G  
 ; Patent No. 6790637  
 ; GENERAL INFORMATION:  
 ; APPLICANT: AMRAD Operations Pcy Ltd  
 ; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2  
 ; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES  
 ; FILE REFERENCE: 2096584  
 ; CURRENT APPLICATION NUMBER: US/09/155,327G  
 ; PRIOR APPLICATION NUMBER: 1999-03-29  
 ; PRIOR FILING DATE: 1996-03-27  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 8  
 ; LENGTH: 581  
 ; TYPE: DNA  
 ; ORGANISM: Mouse  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1) .. (579)  
 US-09-155-327G-8

Query Match 85.9%; Score 501; DB 4; Length 581;  
 Best Local Similarity 91.4%; Pred. No. 8e-123;  
 Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCAAGCTTGGCCCGACAGACACAGGGCTTGTGGAGACTTTGTAGTTAT 60  
 DB 1 ATGCCGACCCCAAGCTTCAACCCAGACACAGCGCTCTAGTGGTACTTTGTAGGCTAT 60  
 QY 61 AAGCTGAGGACAGAGGGTTATGTCTGTGAGCTGGCCCCGGGGAGGGCCCAAGCTGAC 120  
 DB 61 AGGCTGAGGACAGAGGGTTATGTCTGTGAGCTGGGGCTGGGGAAGGCCCAAGCCGCGAC 120  
 QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCCGGCGCAC 180  
 DB 121 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCCGGCGCAC 180  
 QY 181 TTCTCTGATCTGCGCGCTCAGCTGACATGAGTCAAGCCAGCTCAGCCCAAGCAAGCTTCA 240  
 DB 181 TTCTCTGATCTGCGCGCTCAGCTGACATGAGTCAAGCCAGCTCAGCCCAAGCAAGCTTCA 240  
 QY 241 CAGGTCTCCAGCACTTTTCAAGGGGGCCCACTGGGGCCGCTTGAACCTTCTTT 300  
 DB 241 CAGGTCTCCAGCACTTTTCAAGGGGGCCCACTGGGGCCGCTTGAACCTTCTTT 300  
 QY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTCAACAAGAGATGGAACCACTGGTGGGA 360  
 DB 301 GTCTTTGGGGCTGCTGTGTGCTGAGAGTCAACAAGAGATGGAACCACTTTGGTGGGA 360  
 QY 361 CAAGTCAGAGTGTGATGCTGGCTTACCTGAGACACAGTCTGCTGACTGATCCACAGC 420  
 DB 361 CAAGTCAGAGTGTGATGCTGGCTTACCTGAGACACAGTCTGCTGACTGATCCACAGC 420  
 QY 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATAAGGGGACGGGGCCCTGAGAGAGCGCGG 480  
 DB 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATAAGGGGACGGGGCCCTGAGAGAGCGCGG 480  
 QY 481 CGTCTGCGGAGGGGAAGTGGGATCAAGTGAAGACAGTGTGACGGGGCCGTTGGCACTG 540  
 DB 481 CGTCTGCGGAGGGGAAGTGGGATCAAGTGAAGACAGTGTGACGGGGCCGTTGGCACTG 540  
 QY 541 GGGGCCCTGTAACTGTAGGGCCCTTTTGTAGCAAGTG 581  
 DB 541 GGGGCCCTGTAACTGTAGGGCCCTTTTGTAGCAAGTG 581

RESULT 8

US-09-010-147B-23  
 ; Sequence 23, Application US/09010147B  
 ; Patent No. 6653445  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NI et al.  
 ; TITLE OF INVENTION: Human Proteins  
 ; NUMBER OF SEQUENCES: 24  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Human Genome Sciences, Inc.  
 ; STREET: 9410 Key West Avenue  
 ; CITY: Rockville  
 ; STATE: MD  
 ; COUNTRY: USA  
 ; ZIP: 20850  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/010,147B  
 ; FILING DATE: 12-No. 6653445-2002  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/034,205  
 ; FILING DATE: 21-JAN-1997  
 ; APPLICATION NUMBER: US 60/034,204  
 ; FILING DATE: 21-JAN-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Jonathan L. Klein  
 ; REGISTRATION NUMBER: 41,119  
 ; REFERENCE/DOCKET NUMBER: PF353  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 301-309-8504  
 ; TELEFAX: 301-309-8439  
 ; INFORMATION FOR SEQ ID NO: 23:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1098 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..1095  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
 US-09-010-147B-23

Query Match 72.7%; Score 424; DB 4; Length 1098;  
 Best Local Similarity 98.8%; Pred. No. 2.2e-102;  
 Matches 427; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCAAGCTTGGCCCGACAGACACAGGGCTTGTGGAGACTTTGTAGTTAT 60  
 DB 1 ATGGCGACCCCAAGCTTGGCCCGACAGACACAGGGCTTGTGGAGACTTTGTAGTTAT 60  
 QY 61 AAGCTGAGGACAGAGGGTTATGTCTGTGAGCTGGCCCCGGGGAGGGCCCAAGCTGAC 120  
 DB 61 AAGCTGAGGACAGAGGGTTATGTCTGTGAGCTGGCCCCGGGGAGGGCCCAAGCTGAC 120  
 QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCCGGCGCAC 180  
 DB 121 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCCGGCGCAC 180  
 QY 181 TTCTCTGATCTGCGGGCTCAGCTGATGTGACCCAGAGCTCAGCCCAAGCAAGCTTCA 240  
 DB 181 TTCTCTGATCTGCGGGCTCAGCTGATGTGACCCAGAGCTCAGCCCAAGCAAGCTTCA 240  
 QY 241 CAGGTCTCCAGCACTTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCCTTCTTT 300  
 DB 241 CAGGTCTCCAGCACTTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCCTTCTTT 300

QY 301 CTCTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA 360  
 Db 301 GTCTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA 360  
 QY 361 CAAGTCAGAGAGTGTGATGTGGCTTAAGTGAAGACCGCGCTGCTGCACTGATTCACAGC 420  
 Db 361 CAAGTCAGAGAGTGTGATGTGGCTTAAGTGAAGACCGCGCTGCTGCACTGATTCACAGC 420  
 QY 421 AGTGGGGCTGG 432  
 Db 421 AGTGGGGCTGG 432

RESULT 9

US-09-149-476-130  
 / Sequence 130, Application US/09149476  
 / Patent No. 6420526

/ GENERAL INFORMATION:

/ APPLICANT: Rosen et al.  
 / TITLE OF INVENTION: 186 Human Secreted proteins  
 / FILE REFERENCE: P2002P1

/ CURRENT APPLICATION NUMBER: US/09/149,476

/ EARLIER FILING DATE: 1998-09-08

/ EARLIER APPLICATION NUMBER: PCT/US98/04493

/ EARLIER FILING DATE: 1998-03-06

/ EARLIER APPLICATION NUMBER: 60/040,162

/ EARLIER FILING DATE: 1997-03-07

/ EARLIER APPLICATION NUMBER: 60/040,333

/ EARLIER FILING DATE: 1997-03-07

/ EARLIER APPLICATION NUMBER: 60/038,621

/ EARLIER FILING DATE: 1997-03-07

/ EARLIER APPLICATION NUMBER: 60/040,626

/ EARLIER FILING DATE: 1997-03-07

/ EARLIER APPLICATION NUMBER: 60/040,334

/ EARLIER FILING DATE: 1997-03-07

/ EARLIER APPLICATION NUMBER: 60/040,336

/ EARLIER FILING DATE: 1997-03-07

/ EARLIER APPLICATION NUMBER: 60/040,163

/ EARLIER FILING DATE: 1997-03-07

/ EARLIER APPLICATION NUMBER: 60/047,600

/ EARLIER FILING DATE: 1997-05-23

/ EARLIER APPLICATION NUMBER: 60/047,615

/ EARLIER FILING DATE: 1997-05-23

/ EARLIER APPLICATION NUMBER: 60/047,597

/ EARLIER FILING DATE: 1997-05-23

/ EARLIER APPLICATION NUMBER: 60/047,502

/ EARLIER FILING DATE: 1997-05-23

/ EARLIER APPLICATION NUMBER: 60/047,633

/ EARLIER FILING DATE: 1997-05-23

/ EARLIER APPLICATION NUMBER: 60/047,583

/ EARLIER APPLICATION NUMBER: 60/047,582  
 / EARLIER FILING DATE: 1997-05-23  
 / EARLIER APPLICATION NUMBER: 60/047,596  
 / EARLIER FILING DATE: 1997-05-23  
 / EARLIER APPLICATION NUMBER: 60/047,612  
 / EARLIER FILING DATE: 1997-05-23  
 / EARLIER APPLICATION NUMBER: 60/047,632  
 / EARLIER FILING DATE: 1997-05-23  
 / EARLIER APPLICATION NUMBER: 60/047,601  
 / EARLIER FILING DATE: 1997-05-23  
 / EARLIER APPLICATION NUMBER: 60/043,568  
 / EARLIER FILING DATE: 1997-04-11  
 / EARLIER APPLICATION NUMBER: 60/043,314  
 / EARLIER FILING DATE: 1997-04-11  
 / EARLIER APPLICATION NUMBER: 60/043,569  
 / EARLIER FILING DATE: 1997-04-11  
 / EARLIER APPLICATION NUMBER: 60/043,311  
 / EARLIER FILING DATE: 1997-04-11  
 / EARLIER APPLICATION NUMBER: 60/043,671  
 / EARLIER FILING DATE: 1997-04-11  
 / EARLIER APPLICATION NUMBER: 60/043,674  
 / EARLIER FILING DATE: 1997-04-11  
 / EARLIER APPLICATION NUMBER: 60/043,669  
 / EARLIER FILING DATE: 1997-04-11  
 / EARLIER APPLICATION NUMBER: 60/043,312  
 / EARLIER FILING DATE: 1997-04-11  
 / EARLIER APPLICATION NUMBER: 60/043,313  
 / EARLIER FILING DATE: 1997-04-11  
 / EARLIER APPLICATION NUMBER: 60/043,672  
 / EARLIER FILING DATE: 1997-04-11  
 / EARLIER APPLICATION NUMBER: 60/043,315  
 / EARLIER FILING DATE: 1997-04-11  
 / EARLIER APPLICATION NUMBER: 60/048,974  
 / EARLIER FILING DATE: 1997-06-06  
 / EARLIER APPLICATION NUMBER: 60/056,886  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,877  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,889  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,893  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,630  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,878  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,662  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,872  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,882  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,637  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,903  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,888  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,879  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,880  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,894  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,911  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,636  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,874  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,910

EARLIER FILING DATE: 1997-08-22  
 EARLIER APPLICATION NUMBER: 60/056,864  
 EARLIER FILING DATE: 1997-08-22  
 EARLIER APPLICATION NUMBER: 60/056,631  
 EARLIER FILING DATE: 1997-08-22  
 EARLIER APPLICATION NUMBER: 60/056,845  
 EARLIER FILING DATE: 1997-08-22  
 EARLIER APPLICATION NUMBER: 60/056,892  
 EARLIER FILING DATE: 1997-08-22  
 EARLIER APPLICATION NUMBER: 60/057,761  
 EARLIER FILING DATE: 1997-08-22  
 EARLIER APPLICATION NUMBER: 60/047,595  
 EARLIER FILING DATE: 1997-05-23  
 EARLIER APPLICATION NUMBER: 60/047,599  
 EARLIER FILING DATE: 1997-05-23  
 EARLIER APPLICATION NUMBER: 60/047,588  
 EARLIER FILING DATE: 1997-05-23  
 EARLIER APPLICATION NUMBER: 60/047,585  
 EARLIER FILING DATE: 1997-05-23  
 EARLIER APPLICATION NUMBER: 60/047,586  
 EARLIER FILING DATE: 1997-05-23  
 EARLIER APPLICATION NUMBER: 60/047,590  
 EARLIER FILING DATE: 1997-05-23  
 EARLIER APPLICATION NUMBER: 60/047,594  
 EARLIER FILING DATE: 1997-05-23  
 EARLIER APPLICATION NUMBER: 60/047,593  
 EARLIER FILING DATE: 1997-05-23  
 EARLIER APPLICATION NUMBER: 60/047,589  
 EARLIER FILING DATE: 1997-05-23  
 EARLIER APPLICATION NUMBER: 60/047,501  
 EARLIER FILING DATE: 1997-05-23  
 EARLIER APPLICATION NUMBER: 60/043,670  
 EARLIER FILING DATE: 1997-04-11  
 EARLIER APPLICATION NUMBER: 60/043,578  
 EARLIER FILING DATE: 1997-04-11  
 EARLIER APPLICATION NUMBER: 60/043,576  
 EARLIER FILING DATE: 1997-04-11  
 EARLIER APPLICATION NUMBER: 60/047,501  
 EARLIER FILING DATE: 1997-05-23  
 EARLIER APPLICATION NUMBER: 60/043,670  
 EARLIER FILING DATE: 1997-04-11  
 EARLIER APPLICATION NUMBER: 60/056,632  
 EARLIER FILING DATE: 1997-08-22  
 EARLIER APPLICATION NUMBER: 60/056,664  
 EARLIER FILING DATE: 1997-08-22  
 EARLIER APPLICATION NUMBER: 60/056,876  
 EARLIER FILING DATE: 1997-08-22  
 EARLIER APPLICATION NUMBER: 60/056,881  
 EARLIER FILING DATE: 1997-08-22  
 EARLIER APPLICATION NUMBER: 60/056,909  
 EARLIER FILING DATE: 1997-08-22  
 EARLIER APPLICATION NUMBER: 60/056,875  
 EARLIER FILING DATE: 1997-08-22  
 EARLIER APPLICATION NUMBER: 60/056,862  
 EARLIER FILING DATE: 1997-08-22  
 EARLIER APPLICATION NUMBER: 60/056,887  
 EARLIER FILING DATE: 1997-08-22  
 EARLIER APPLICATION NUMBER: 60/056,908  
 EARLIER FILING DATE: 1997-08-22  
 EARLIER APPLICATION NUMBER: 60/048,964  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/057,650  
 EARLIER FILING DATE: 1997-09-05  
 EARLIER APPLICATION NUMBER: 60/056,884  
 EARLIER FILING DATE: 1997-08-22  
 EARLIER APPLICATION NUMBER: 60/057,669  
 EARLIER FILING DATE: 1997-09-05  
 EARLIER APPLICATION NUMBER: 60/049,610  
 EARLIER FILING DATE: 1997-06-13  
 EARLIER APPLICATION NUMBER: 60/061,060  
 EARLIER FILING DATE: 1997-10-02

Query Match 72.7%; Score 423.6; DB 3; Length 1864;  
 Best Local Similarity 98.6%; Pred. No. 3.3e-102;  
 Matches 426; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACAGGGCTCTGTGGCAGACTTTGTAGGTTAT 60  
 DB 11 ATGGCGACCCAGCCTCGGCCCCAGACACAGGGCTCTGTGGCAGACTTTGTAGGTTAT 70  
 QY 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 120  
 DB 71 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 130  
 QY 121 CCGCTGACCAAGCCATGCGGCGAGCTGAGATGATTGAGACCCGCTTCCGGCGCACC 180  
 DB 131 CCGCTGACCAAGCCATGCGGCGAGCTGAGATGATTGAGACCCGCTTCCGGCGCACC 190  
 QY 181 TTCTGTATCTGCGGCTCAGCTGATGACCCAGGCTCAGCCAGCAAGCCTTACC 240  
 DB 191 TTCTGTATCTGCGGCTCAGCTGATGACCCAGGCTCAGCCAGCAAGCCTTACC 250  
 QY 241 CAGCTCTCCGACGAATTTTCAAGGGGCCCCCACTGGGGCCGCTTGTAGCCTTCTT 300  
 DB 251 CAGCTCTCCGACGAATTTTCAAGGGGCCCCCACTGGGGCCGCTTGTAGCCTTCTT 310  
 QY 301 CTCTTTGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAAACCACTGTTGGA 360  
 DB 311 GTCTTTGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAAACCACTGTTGGA 370  
 QY 361 CAAGTGACAGAGTGATGTGCTGCTTACTGAGACGCGGCTGTGATGATCCACAGC 420  
 DB 371 CAAGTGACAGAGTGATGTGCTGCTTACTGAGACGCGGCTGTGATGATCCACAGC 430  
 QY 421 AGTGGGGGCTGG 432  
 DB 431 AGTGGGGGCTGG 442

RESULT 10  
 US-09-949-016-16799  
 ; Sequence 16799, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; PRIOR FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 16799  
 ; LENGTH: 5199  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-16799

Query Match 72.6%; Score 423.4; DB 4; Length 5199;  
 Best Local Similarity 98.6%; Pred. No. 5.3e-102;  
 Matches 427; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 ATGGGACCCAGCCTCGGCCCCAGACACAGGGCTCTGTGGCAGACTTTGTAGGTTAT 60  
 DB 2001 ATGGGACCCAGCCTCGGCCCCAGACACAGGGCTCTGTGGCAGACTTTGTAGGTTAT 2060  
 QY 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 120  
 DB 2061 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 2120  
 QY 121 CCGCTGACCAAGCCATGCGGCGAGCTGAGATGATTGAGACCCGCTTCCGGCGCACC 180

Db 2121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTGAGACCCCGCTTCCGGCGCACC 2180  
QY 181 TTCTTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
Db 2181 TTCTTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 2240  
QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCCACTGGGGGGCGGCTTGTAGCCTTCTTT 300  
Db 2241 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCCCACTGGGGGGCGGCTTGTAGCCTTCTTT 2300  
QY 301 CTCTTTGGGGCTGCACCTGTGTCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 360  
Db 2301 GTCTTTGGGGCTGCACCTGTGTCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 2360  
QY 361 CAAGTGACGAGATGATGGTGGCTTACCTGAGACCGCGGCTGTGCTGATGATCCACAGC 420  
Db 2361 CAAGTGACGAGATGATGGTGGCTTACCTGAGACCGCGGCTGTGCTGATGATCCACAGC 2420  
QY 421 AGTGGGGGCTGGG 433  
Db 2421 AGTGGGGGCTGGG 2433

RESULT 11  
US-09-949-016-177003  
; Sequence 177003, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 177003  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-177003

Query Match 71.1%; Score 414.6; DB 4; Length 601;  
Best Local Similarity 98.6%; Pred. No. 5.4e-100;  
Matches 417; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCGAGCTCGGCCCCAGACACAGCGGCTCTGTGGCAGACTTTGTAGGTTAT 60  
Db 179 ATGGCGACCCCGAGCTCGGCCCCAGACACAGCGGCTCTGTGGCAGACTTTGTAGGTTAT 238  
QY 61 AAGCTGAGGACAGAGGGTTATGTCTGTGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC 120  
Db 239 AAGCTGAGGACAGAGGGTTATGTCTGTGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC 298  
QY 121 CCGGTGACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCGGCTTCGGGCGCAC 180  
Db 299 CCRCTGACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCGGCTTCGGGCGCAC 358  
QY 181 TTCTTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
Db 359 TTCTTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 418  
QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCCACTGGGGGGCGGCTTGTAGCCTTCTTT 300  
Db 419 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCCCACTGGGGGGCGGCTTGTAGCCTTCTTT 478  
QY 301 CTCTTTGGGGCTGCACCTGTGTCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 360

Db 479 GTCTTTGGGGCTGCACCTGTGTCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 538  
QY 361 CAAGTGACGAGATGATGGTGGCTTACCTGAGACCGCGGCTGTGCTGATGATCCACAGC 420  
Db 539 CAAGTGACGAGATGATGGTGGCTTACCTGAGACCGCGGCTGTGCTGATGATCCACAGC 598  
QY 421 AGT 423  
Db 599 AGT 601

RESULT 12  
US-08-081-448-5  
; Sequence 5, Application US/08081448  
; Patent No. 5646008  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Craig B.  
; APPLICANT: Boise, Lawrence H.  
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:  
; TITLE OF INVENTION: Compositions and Methods  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. 5646008th Clark Street, Suite 800  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/081,448  
; FILING DATE: 19930622  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5646008thrup, Thomas E.  
; REGISTRATION NUMBER: 33,268  
; REFERENCE/DOCKET NUMBER: ARCD090  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-744-0090  
; TELEFAX: 312-755-4489  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 926 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 135..836  
US-08-081-448-5

Query Match 22.5%; Score 131; DB 1; Length 926;  
Best Local Similarity 56.3%; Pred. No. 5.3e-25;  
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 98 CCGGGAGGGGCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGT 157  
Db 364 CCGGGAGGGTGATCCCATGCGAGCAGTAAGCAAGCGCTGAGGGAGCGAGCGAGT 423  
QY 158 TCGAAGCCGCTTCCGGCGCACCTTCTGATCTGGCGGCTCAGCTGCATGAGACCCAG 217  
Db 424 TTGAAGTGGGTACCGCGCGGCATTTCACTGACCTGACATCCAGCTCCATCAACCCAG 483  
QY 218 GGTACGCCAGCAACGCTTCAACCCAGGCTTCCGACGAACCTTTTCAAGGGGGCCCCAACT 277  
Db 484 GGACAGCATATCAAGACTTTTGAACAGGTAGTGAATGAACCTTCCGGGATGGGTAACCT 543



[illegible]

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RESULT 13
US-08-470-670A-6
; Sequence 6, Application US/08470670A
; Patent No. 5834309
; Patent No. 5834309 5710045
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B. B.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,670A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,448
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:090--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
US-08-470-670A-6

Query Match      22.5%; Score 131; DB 2; Length 926;
Best Local Similarity 56.3%; Pred. No. 5.3e-25;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0

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[illegible]

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RESULT 14
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; Sequence 1, Application US/08481739
; Patent No. 6143291
; GENERAL INFORMATION:
; APPLICANT: June, Carl H. and Thompson, Craig B.
; TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
; TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,739
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,518
; FILING DATE: 04-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. (GAD)
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: RPI-034CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 135..836  
US-08-481-739-1

Query Match 22.5%; Score 131; DB 3; Length 926;  
Best Local Similarity 56.3%; Pred. No. 5.3e-25;  
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

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DB 364 CCGGGAGGTGATCCCATGCGACAGTAAGCAAGCGCTGAGGAGGCAAGCGAGT 423  
QY 158 TCGAGACCCGCTCCGGCGCACCTTCTGTATCTGGCGCTCAGCTGATGACCCAG 217  
DB 424 TTGAAGTGGGTACCGGCGGATTCAGTGAACCTGACATCCAGCTCCACATCACCAG 483  
QY 218 GCTCAGCCCAAGCAAGCTTCAACCCAGTCTCCGACGAACCTTTTCAAGGGGCCCCA 277  
DB 484 GACAGCATATCAGAGCTTGAACAGGTAGTGAATGAATCTTCCGGATGGGTAACT 543  
QY 278 GGGGCGCCTTGTAGCCTTCTTCTTTGGGGCTGCACCTGTGTGCTGAGATGACA 337  
DB 544 GGGGTGCAATGTGGCTTTTCTCTTCCGCGGCGGCTGCGTGAAGCGTAGACA 603  
QY 338 AGGAGTGAACCACTGTGGGACAGTGCAGAGTGAATGTGGCTTACCTGAGACGC 397  
DB 604 AGGAGTGAAGTATTGTGTGATGCGATGCGAGCTTGAATGCCACTTACCTGAATGAC 663  
QY 398 GGTGTGCACTGTGATCCACAGAGTGGGGCTGGCGGAGTTCAAGCTCTAATACGGG 457  
DB 664 ACCTAGAGCCTTGTATCCAGAGAACGGCGCTGGATCTTTGTGAACCTATAGGA 723  
QY 458 ACGGGCCCTGAGAGAGCGCGGCTGTGCGGAGGGAAGTGGCATCAGTGAAGACAG 517  
DB 724 ACAATGCAAGCAGCCGAGAGCGGAAGGCCAGGAACGCTTCAACCGCTGCTCTGACGG 783  
QY 518 TGCTGACGGGGGCGG 532  
DB 784 GCATGACTGTGGCGG 798

RESULT 15  
US-09-167-921-1  
Sequence 1, Application US/09167921A  
Patent No. 6172216  
GENERAL INFORMATION:  
APPLICANT: Bennett, C. Frank  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Monia, Brett P.  
APPLICANT: Nickoloff, Brian J.  
APPLICANT: Zhang, Qingqing  
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
FILE REFERENCE: ISPH-0324  
CURRENT APPLICATION NUMBER: US/09/167,921A  
CURRENT FILING DATE: 1998-10-07  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 926  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (135)..(836)  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: L20121 Genbank  
DATABASE ENTRY DATE: 1994-07-26  
US-09-167-921-1

Query Match 22.5%; Score 131; DB 3; Length 926;  
Best Local Similarity 56.3%; Pred. No. 5.3e-25;

Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;  
QY 98 CCGGGAGGGCCCAAGCTGACCCGCTGCAACCAAGCCATGCGGAGCTGAGATGAGT 157  
DB 364 CCGGGAGGTGATCCCATGCGACAGTAAGCAAGCGCTGAGGAGGCAAGCGAGT 423  
QY 158 TCGAGACCCGCTCCGGCGCACCTTCTGTATCTGGCGCTCAGCTGATGACCCAG 217  
DB 424 TTGAAGTGGGTACCGGCGGATTCAGTGAACCTGACATCCAGCTCCACATCACCAG 483  
QY 218 GCTCAGCCCAAGCAAGCTTCAACCCAGTCTCCGACGAACCTTTTCAAGGGGCCCCA 277  
DB 484 GACAGCATATCAGAGCTTGAACAGGTAGTGAATGAATCTTCCGGATGGGTAACT 543  
QY 278 GGGGCGCCTTGTAGCCTTCTTCTTTGGGGCTGCACCTGTGTGCTGAGATGACA 337  
DB 544 GGGGTGCAATGTGGCTTTTCTCTTCCGCGGCGGCTGCGTGAAGCGTAGACA 603  
QY 338 AGGAGTGAACCACTGTGGGACAGTGCAGAGTGAATGTGGCTTACCTGAGACGC 397  
DB 604 AGGAGTGAAGTATTGTGTGATGCGATGCGAGCTTGAATGCCACTTACCTGAATGAC 663  
QY 398 GGTGTGCACTGTGATCCACAGAGTGGGGCTGGCGGAGTTCAAGCTCTAATACGGG 457  
DB 664 ACCTAGAGCCTTGTATCCAGAGAACGGCGCTGGATCTTTGTGAACCTATAGGA 723  
QY 458 ACGGGCCCTGAGAGAGCGCGGCTGTGCGGAGGGAAGTGGCATCAGTGAAGACAG 517  
DB 724 ACAATGCAAGCAGCCGAGAGCGGAAGGCCAGGAACGCTTCAACCGCTGCTCTGACGG 783  
QY 518 TGCTGACGGGGGCGG 532  
DB 784 GCATGACTGTGGCGG 798

Search completed: April 10, 2005, 20:17:21  
Job time : 146.247 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 18:38:08 ; Search time 500.358 Seconds  
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7060.905 Million cell updates/sec

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Perfect score: 583  
Sequence: 1 atggcgaccaccagctcgcc.....cttttctagcaagtgaa 583

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	578.2	99.2	583	US-09-925-674A-6	Sequence 6, Appli
2	577.2	99.0	582	US-10-384-339C-37	Sequence 37, Appli
3	572.4	98.2	582	US-10-479-832A-4	Sequence 4, Appli
4	519.6	89.1	582	US-09-925-674A-8	Sequence 8, Appli
5	423.6	72.7	1864	US-09-809-391-130	Sequence 130, App
6	423.6	72.7	1864	US-09-882-171-130	Sequence 130, App
7	423.6	72.7	1864	US-10-164-861-130	Sequence 130, App
8	423.4	72.6	578	US-10-029-386-10549	Sequence 10549, A
9	422.4	72.5	433	US-10-029-386-24249	Sequence 24249, A
10	255.4	43.8	6049	US-10-311-455-201	Sequence 201, App
11	219.8	37.7	6049	US-10-311-455-202	Sequence 202, App

12	152	26.1	590	16	US-10-029-386-13384	Sequence 13384, A
13	151	25.9	151	16	US-10-029-386-27084	Sequence 27084, A
14	150	25.7	150	9	US-09-864-761-17690	Sequence 17690, A
15	145.2	24.9	660	17	US-10-402-017-9	Sequence 9, Appli
16	144.2	24.7	600	17	US-10-402-017-7	Sequence 9, Appli
17	141.2	24.2	540	17	US-10-402-017-5	Sequence 5, Appli
18	136.2	23.4	660	17	US-10-402-017-11	Sequence 11, Appli
19	136.2	23.4	660	17	US-10-402-017-3	Sequence 3, Appli
20	136.2	23.4	660	17	US-10-402-017-3	Sequence 3, Appli
21	131	22.5	1466	18	US-10-283-975A-394	Sequence 394, App
22	131	22.5	636	16	US-10-169-223-13	Sequence 13, Appli
23	131	22.5	702	10	US-09-959-987-9	Sequence 9, Appli
24	131	22.5	926	9	US-09-734-847A-39	Sequence 39, Appli
25	131	22.5	926	9	US-09-734-847A-39	Sequence 39, Appli
26	131	22.5	926	15	US-10-072-830-3	Sequence 3, Appli
27	131	22.5	926	16	US-10-302-262-1	Sequence 1, Appli
28	131	22.5	926	17	US-10-402-017-1	Sequence 1, Appli
29	131	22.5	926	17	US-10-641-643-1430	Sequence 1430, Ap
30	131	22.5	926	18	US-10-717-597-87	Sequence 87, Appli
31	131	22.5	926	18	US-10-776-827-106	Sequence 106, App
32	131	22.5	926	18	US-10-825-282-47	Sequence 47, Appli
33	131	22.5	926	19	US-10-479-832A-3	Sequence 3, Appli
34	131	22.5	926	18	US-10-792-517-1	Sequence 1, Appli
35	129.8	22.3	1748	17	US-10-388-934-539	Sequence 539, App
36	129.8	22.3	1748	17	US-10-388-934-539	Sequence 539, App
37	127.6	21.9	1455	18	US-10-792-517-7	Sequence 7, Appli
38	126.6	21.7	711	13	US-10-087-192-1952	Sequence 1952, Ap
39	125	21.4	720	17	US-10-148-953A-8	Sequence 8, Appli
40	123.4	21.2	717	16	US-10-053-645A-20	Sequence 20, Appli
41	123.4	21.2	720	17	US-10-148-953A-6	Sequence 6, Appli
42	123.4	21.2	720	17	US-10-148-953A-7	Sequence 7, Appli
43	123.4	21.2	720	17	US-10-297-321-1	Sequence 1, Appli
44	123.4	21.2	931	18	US-10-714-310-18	Sequence 18, Appli
45	123.4	21.2	5086	8	US-08-726-211-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-09-925-674A-6  
; Sequence 6, Application US/09925674A  
; Patent No. US20020119943A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES  
; FILE REFERENCE: 11686A  
; CURRENT APPLICATION NUMBER: US/09/925, 674A  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/925, 674  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: PN8965  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 583  
; TYPE: DNA  
; ORGANISM: HUMAN  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(579)  
US-09-925-674A-6

Query Match 99.2%; Score 578.2; DB 9; Length 583;  
Best local Similarity 99.5%; Pred. No. 1.2e-156;  
Matches 580; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY : 1 ATGGCGACCCAGCCTCGGCCAGACACACGGGCTGTGTGCACACTTTGTAGTTAT 60  
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Db 121 CCGCTGCACCAAGCCATGCGGAGCTGAGATGAGTTGAGACCCGCTTCCGGCGCAC 180
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QY 301 CTCTTTGGGGCTGCACCTGTGTCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 360
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RESULT 2
US-10-384-339C-37
; Sequence 37, Application US/10384339C
; Publication No. US20040175703A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Roland
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GE
; FILE REFERENCE: 20200/2002
; CURRENT APPLICATION NUMBER: US/10/384,339C
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/EP02/00152
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: DE 10155280.7
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: DE 10158411.3
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: DE 10160151.4
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; TITLE: bcl-w
; PATENT DOCUMENT NUMBER: U59747
US-10-384-339C-37

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Query Match 99.0%; Score 577.2; DB 18; Length 582;
Best Local Similarity 99.5%; Pred. No. 2.3e-156;
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGGGCAACCCAGCCTCGGCCCAAGACACACGGGCTCTGTGGCAGACTTTGTAGTTAT 60

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Db 1 ATGGGCAACCCAGCCTCGGCCCAAGACACACGGGCTCTGTGGCAGACTTTGTAGTTAT 60
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QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAACGCTTACC 240
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QY 361 CAAGTCAGAGAGTGATGGTGGCCCTACCTGAGACGCGGCTGTGCACTGATCCACAGC 420
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RESULT 3
US-10-479-832A-4
; Sequence 4, Application US/10479832A
; Publication No. US20050064407A1
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson Research Pty Ltd
; TITLE OF INVENTION: bcl-2 DNazymes
; FILE REFERENCE: WJPI3107942
; CURRENT APPLICATION NUMBER: US/10/479,832A
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-479-832A-4

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Query Match 98.2%; Score 572.4; DB 19; Length 582;
Best Local Similarity 99.0%; Pred. No. 5.5e-155;
Matches 576; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Qy 241 CAGGCTCCGACGAATTTTCAAGGGGCGCCCACTGGGGCCCTTGAGCTTCTTT 300
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Db 241 CAGGCTCCGACGAATTTTCAAGGGGCGCCCACTGGGGCCCTTGAGCTTCTTT 300
Qy 301 CTCTTTGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAACCACTGGTGGGA 360
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Db 301 GTCTTTGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAACCACTGGTGGGA 360
Qy 361 CAAGTGCAGAGTTGATGTGTGGCTTACCTGAGACGCGGCTGTGCTGATCCACAGC 420
    |||
Db 361 CAAGTGCAGAGTTGATGTGTGGCTTACCTGAGACGCGGCTGTGCTGATCCACAGC 420
Qy 421 AGTGGGGGCTGGGCGGAGTTCAACAGCTCTATACGGGGACGGGGCCCTGGAGAGGCGCGG 480
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Db 421 AGTGGGGGCTGGGCGGAGTTCAACAGCTCTATACGGGGACGGGGCCCTGGAGAGGCGCGG 480
Qy 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCGTGGCACTG 540
    |||
Db 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCGTGGCACTG 540
Qy 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTGA 582
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Db 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTGA 582
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## RESULT 4

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US-09-925-674A-8
; Sequence 8, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(579)
US-09-925-674A-8
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Query Match 89.1%; Score 519.6; DB 9; Length 582;
Best Local Similarity 93.3%; Pred. No. 9, 1e-140;
Matches 543; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT 60
    |||
Db 1 ATGGCGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Qy 61 AAGTGAGGACAGAGGTTATGTCTGTGAGCTGCCCCGGGGAGGGGCCAGCAGCTGAC 120
    |||
Db 61 AAGTGAGGACAGAGGTTATGTCTGTGAGCTGCCCCGGGGAGGGGCCAGCAGCTGAC 120
Qy 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCGGCGCACC 180
    |||
Db 121 CCGCTGACCAAGCCATGCGGGCTGTGAGAGAGATTGAGACCCGCTTCGGCGCACC 180
Qy 181 TTCTCTGATCTGGGCGCTCAGCTGCATGTGACCCCAAGGCTCAGCCAGCAAGCTTCACC 240
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Db 181 TTCTCTGACTGGCCCGCTCAGCTTACACGTGACCCCAAGGCTCAGCCAGCAAGCTTCACC 240
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Qy 241 CAGGCTCCGACGAATTTTCAAGGGGCGCCCACTGGGGCCCTTGAGCTTCTTT 300
    |||
Db 241 CAGGTTCCGACGAATTTTCCAAAGGGGCGCCCACTGGGGCCCTTGAGCTTCTTT 300
Qy 301 CTCTTTGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAACCACTGGTGGGA 360
    |||
Db 301 GTCTTTGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGAGCTTTGGTGGGA 360
Qy 361 CAAGTGCAGAGTTGATGTGTGAGGCTTACCTGAGACGCGGCTGTGCTGATCCACAGC 420
    |||
Db 361 CAAGTGCAGAGTTGATGTGTGAGGCTTACCTGAGACACAGCTGTGCTGATCCACAGC 420
Qy 421 AGTGGGGGCTGGGCGGAGTTCAACAGCTCTATACGGGGACGGGGCCCTGGAGAGGCGCGG 480
    |||
Db 421 AGTGGGGGCTGGGCGGAGTTCAACAGCTCTATACGGGGACGGGGCCCTGGAGAGGCGCGG 480
Qy 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCGTGGCACTG 540
    |||
Db 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCGTGGCACTG 540
Qy 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTGA 582
    |||
Db 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTGA 582
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## RESULT 5

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US-09-809-391-130
; Sequence 130, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 130
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1648)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-809-391-130
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Query Match 72.7%; Score 423.6; DB 10; Length 1864;
Best Local Similarity 98.6%; Pred. No. 4, 7e-112;
Matches 426; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT 60
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Db 11 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT 70
Qy 61 AAGTGAGGACAGAGGTTATGTCTGTGAGCTGCCCCGGGGAGGGGCCAGCAGCTGAC 120
    |||
Db 71 AAGTGAGGACAGAGGTTATGTCTGTGAGCTGCCCCGGGGAGGGGCCAGCAGCTGAC 130
Qy 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCGGCGCACC 180
    |||
Db 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCGGCGCACC 180
Qy 181 TTCTCTGATCTGGGCGCTCAGCTGCATGTGACCCCAAGGCTCAGCCAGCAAGCTTCACC 240
    |||
Db 181 TTCTCTGATCTGGGCGCTCAGCTGCATGTGACCCCAAGGCTCAGCCAGCAAGCTTCACC 240
Qy 241 CAGGCTCCGACGAATTTTCAAGGGGCGCCCACTGGGGCCCTTGAGCTTCTTT 300
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Db 251 CAGTCTCCGATGAACCTTTTCAAGGGGCCCCCACTGGGGCCCTTGTAGCCTTCTTT 310  
QY 301 CTCTTTGGGGCTGCACTGTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 360  
Db 311 GTCTTTGGGGCTGCACTGTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 370  
QY 361 CAAGTCAGAGAGTGTGTGTGCTTACCTGAGACCGCGCTGTGTGACTGTGATCCAGAC 420  
Db 371 CAAGTCAGAGAGTGTGTGTGCTTACCTGAGACCGCGCTGTGTGACTGTGATCCAGAC 430  
QY 421 AGTGGGGGCTGG 432  
Db 431 AGTGGGGGCTGG 442

RESULT 6  
US-09-882-171-130

/ Sequence 130, Application US/09882171  
/ Publication No. US20030175858A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Ruben et al.  
/ TITLE OF INVENTION: 186 Human Secreted proteins  
/ FILE REFERENCE: P2002P2  
/ CURRENT APPLICATION NUMBER: US/09/882,171  
/ PRIOR FILING DATE: 2001-06-18  
/ PRIOR APPLICATION NUMBER: 09/809,391  
/ PRIOR FILING DATE: 2001-03-16  
/ PRIOR APPLICATION NUMBER: 09/149,476  
/ PRIOR FILING DATE: 1998-09-08  
/ PRIOR APPLICATION NUMBER: PCT/US98/04493  
/ PRIOR FILING DATE: 1998-03-06  
/ PRIOR APPLICATION NUMBER: 60/040,162  
/ PRIOR FILING DATE: 1997-03-07  
/ PRIOR APPLICATION NUMBER: 60/040,333  
/ PRIOR FILING DATE: 1997-03-07  
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/ PRIOR FILING DATE: 1997-03-07  
/ PRIOR APPLICATION NUMBER: 60/040,336  
/ PRIOR FILING DATE: 1997-03-07  
/ PRIOR APPLICATION NUMBER: 60/040,163  
/ PRIOR FILING DATE: 1997-03-07  
/ PRIOR APPLICATION NUMBER: 60/047,600  
/ PRIOR FILING DATE: 1997-05-23  
/ PRIOR APPLICATION NUMBER: 60/047,615  
/ PRIOR FILING DATE: 1997-05-23  
/ PRIOR APPLICATION NUMBER: 60/047,597  
/ PRIOR FILING DATE: 1997-05-23  
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/ PRIOR APPLICATION NUMBER: 60/048,974  
/ PRIOR FILING DATE: 1997-06-06  
/ PRIOR APPLICATION NUMBER: 60/056,886  
/ PRIOR FILING DATE: 1997-08-22  
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;; PRIOR FILING DATE: 1997-06-06  
;; PRIOR APPLICATION NUMBER: 60/057,650  
;; PRIOR FILING DATE: 1997-09-05  
;; PRIOR APPLICATION NUMBER: 60/056,884  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/057,669  
;; PRIOR FILING DATE: 1997-09-05

Query Match 72.7%; Score 423.6; DB 10; Length 1864;

Best Local Similarity 98.6%; Pred. No. 4.7e-112;  
Matches 426; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 1 ATGGCGACCCAGCCTCGGCCACAGACACGGGCTCTGTGGCAGACTTTGTAGTTAT 60  
DB 11 ATGGCGACCCAGCCTCGGCCACAGACACGGGCTCTGTGGCAGACTTTGTAGTTAT 70  
QY 61 AAGCTGAGCAGAAAGGTTATGTCGTGAGCTGGCCCCGGGAGGCCCCAGAGCTGAC 120  
DB 71 AAGCTGAGCAGAAAGGTTATGTCGTGAGCTGGCCCCGGGAGGCCCCAGAGCTGAC 130  
QY 121 CCGCTGACCAAGCCATGCGGGCAGCTGGAGATGATGATTGAGACCCGCTTCCGGCGACC 180  
DB 131 CCGCTGACCAAGCCATGCGGGCAGCGAGAGATGATTGAGACCCGCTTCCGGCGACC 190  
QY 181 TTCTGTGATCTGGCGGCTCAGCTGCATGTGACCCCAAGGCTCAGCCCAACAGCTTACC 240  
DB 191 TTCTGTGATCTGGCGGCTCAGCTGCATGTGACCCCAAGGCTCAGCCCAACAGCTTACC 250  
QY 241 CAGGTCTCCGACCACTTTTCAAGGGGGCCCCCACTGGGGCCGCTTGTAGCCTCTTT 300  
DB 251 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCCCACTGGGGCCGCTTGTAGCCTCTTT 310  
QY 301 CTCCTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAAGAGATGAAACCACTGTGGGA 360  
DB 311 GTCCTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAAGAGATGAAACCACTGTGGGA 370  
QY 361 CAAGTCAGAGAGTGATGTGGCTTACCTGAGACGCGGCTGTGCTGATCCACAGC 420  
DB 371 CAAGTCAGAGAGTGATGTGGCTTACCTGAGACGCGGCTGTGCTGATCCACAGC 430  
QY 421 AGTGGGGCTGG 432  
DB 431 AGTGGGGCTGG 442

RESULT 7  
US-10-164-861-130  
; Sequence 130, Application US/10164861  
; Publication No. US20030225248A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/10/164,861  
; PRIOR FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: US/09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 757  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 130  
; LENGTH: 1864  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1648)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-10-164-861-130

Query Match 72.7%; Score 423.6; DB 17; Length 1864;  
Best Local Similarity 98.6%; Pred. No. 4.7e-112;  
Matches 426; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 1 ATGGCGACCCAGCCTCGGCCACAGACACGGGCTCTGTGGCAGACTTTGTAGTTAT 60  
DB 11 ATGGCGACCCAGCCTCGGCCACAGACACGGGCTCTGTGGCAGACTTTGTAGTTAT 70  
QY 61 AAGCTGAGCAGAAAGGTTATGTCGTGAGCTGGCCCCGGGAGGCCCCAGAGCTGAC 120  
DB 71 AAGCTGAGCAGAAAGGTTATGTCGTGAGCTGGCCCCGGGAGGCCCCAGAGCTGAC 130

QY	181	TTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCCAACGCTTACC	240
Db	285	TTCTGTATGTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCCAACGCTTACC	240
QY	241	CAGSTCTCGACGAACCTTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCTTCTTT	344
Db	345	CAGSTCTCCGATGAACCTTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCTTCTTT	300
QY	301	CTCTTTGGGGCTGCACTGTGTGTGACAGTGTCAACAAGAGATGAACCACTGGTGA	404
Db	405	GTCTTTGGGGCTGCACTGTGTGTGACAGTGTCAACAAGAGATGAACCACTGGTGA	360
QY	361	CAAGTGACGAGTGTGATGTGGCTTACCTGGAGACGCGGCTGTGTGACTGTGATCCACAGC	464
Db	465	CAAGTGACGAGTGTGATGTGGCTTACCTGGAGACGCGGCTGTGTGACTGTGATCCACAGC	420
QY	421	AGTGGGGGCTGGG	433
Db	525	AGTGGGGGCTGGG	537

Query	Match	Best Local Similarity	72.6%	Score 423.4	DB 16	Length 578
Matches 427	Conservative	0	Mismatches 6	Indels 0	Gaps 0	
Db	1	ATGGCGACCCCGAGCTCTGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT	60			
QY	105	ATGGCGACCCCGAGCTCTGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT	60			
Db	61	AAGCTGAGGCAGAGGGTTATGTCTGTGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC	164			
QY	165	AAGCTGAGGCAGAGGGTTATGTCTGTGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC	120			
Db	121	CCGCTGCACCAAGCCATGCGGGCAGCTGGAATGATTCGAGACCCGCTTCGGCGCACCC	224			
QY	225	CCGCTGCACCAAGCCATGCGGGCAGCTGGAATGATTCGAGACCCGCTTCGGCGCACCC	180			
Db			284			

Query Match	Best Local Similarity	72.5%;	Score 422.4;	DB 16;	Length 433;
Matches 426;	Conservative	0;	Mismatches 6;	Indels 0;	Gaps
QY	1	ATGGCGACCCCGAGCTCGGCCCGACACACACCGGCTCTGTGGCAGACTTTGTAAGTTAT			60
Db	2	ATGGCGACCCCGAGCTCGGCCCGACACACACCGGCTCTGTGGCAGACTTTGTAAGTTAT			60
QY	61	AAGCTGAGCGCAGAAGGTTATGTCTGTGAGCTGGCCCCGGGAGGCGCCACGAGCTGAC			61
Db	62	AAGCTGAGCGCAGAAGGTTATGTCTGTGAGCTGGCCCCGGGAGGCGCCACGAGCTGAC			120
QY	121	CCGCTGCACCAAGCCCATGCGGGCAGCTGGAGATGACTTCAGACCCGCTTCCGGCGCACCC			121
Db	122	CCGCTGCACCAAGCCCATGCGGGCAGCTGGAGATGACTTCAGACCCGCTTCCGGCGCACCC			180
QY	181	TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCGAGCTCAGCCAGCAACGCTTCACC			181
Db	182	TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCGAGCTCAGCCAGCAACGCTTCACC			240



QY 241 CAGGTCTCCGACGAATTTTCAAGGGGGCCCCAATGGGGCCGCTTGTAGCTTCTTT 300  
DB 242 CAGGTCTCCGATGAATTTTCAAGGGGGCCCCAATGGGGCCGCTTGTAGCTTCTTT 301  
QY 301 CTCTTTGGGGCTGCACTGTGTGTGAGAGTGTCAACAAGAGATGAACCACTGGTGGGA 360  
DB 302 GTCTTTGGGGCTGCACTGTGTGTGAGAGTGTCAACAAGAGATGAACCACTGGTGGGA 361  
QY 361 CAAGTGACAGAGTGTGATGTGGCTTACCTGAGACGCGGCTGTGACTGATCCACAGC 420  
DB 362 CAAGTGACAGAGTGTGATGTGGCTTACCTGAGACGCGGCTGTGACTGATCCACAGC 421  
QY 421 AGTGGGGGCTGG 432  
DB 422 AGTGGGGGCTGG 433

## RESULT 10

US-10-311-455-201  
; Sequence 201, Application US/10311455  
; Publication No. US20030143606A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ  
; TITLE OF INVENTION: cytosine methylation  
; FILE REFERENCE: 5013.1014  
; CURRENT APPLICATION NUMBER: US/10/311,455  
; CURRENT FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: PCT/EP01/07537  
; PRIOR FILING DATE: 2001-07-02  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 2424  
; SEQ ID NO 201  
; LENGTH: 6049  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-311-455-201

Query Match 43.8%; Score 255.4; DB 15; Length 6049;  
Best Local Similarity 74.4%; Pred. No. 1.6e-63;  
Matches 322; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 1 ATGGGACCCGACCTCGGCCCCAGACACAGGGGCTCTGTGTGACAGACTTTAGATTAT 60  
DB 5001 ATGGCGATTTTAGTTCCGTTTATAGATATACGGGTTTGTGTGATGTTAGATTAT 5060  
QY 61 AAGCTGAGGAGAGGGTTATGTCTGTGAGCTGGCCCCCGGGAGGGGCCACAGACTGAC 120  
DB 5061 AAGTTGAGGTAGAGGGTTATGTCTGTGAGCTGGCCCCCGGGAGGGGTTAGATTAT 5120  
QY 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCCGGCGCACC 180  
DB 5121 TCCTGTATTAAGTTATGCGGGTAGTTGAGATGAGTTGAGATTCTTTTCCGGCTATT 5180  
QY 181 TTCTCTGATCTGGGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 240  
DB 5181 TTTTGTGATTTGGGGCTTAGTTGATGTGATTTAGGTTTATTAATTAACGTTTATT 5240  
QY 241 CAGGTCTCCGACGAATTTTCAAGGGGGCCCCAATGGGGCCGCTTGTAGCTTCTTT 300  
DB 5241 TAGGTTTTCGATGAATTTTAAAGGGGTTTAAATGGGGCTGTTTGTAGTTTCTTTT 5300  
QY 301 CTCTTTGGGGCTGCACTGTGTGTGAGAGTGTCAACAAGAGATGAACCACTGGTGGGA 360  
DB 5301 GTTTTGGGGTGTGATGTGTGTGAGAGTGTAAATAAGAGATGAATTAATTGGTGGGA 5360

QY 361 CAAGTGACAGAGTGTGATGTGGCTTACCTGAGACGCGGCTGTGACTGATCCACAGC 420  
DB 5361 TAAGTGTAGAGTGTGATGTGTTTATTTGAGAGACGTAGTTGTTGATTTAGT 5420  
QY 421 AGTGGGGGCTGG 433  
DB 5421 AGTGGGGGCTGG 5433

## RESULT 11

US-10-311-455-202/c  
; Sequence 202, Application US/10311455  
; Publication No. US20030143606A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ  
; TITLE OF INVENTION: cytosine methylation  
; FILE REFERENCE: 5013.1014  
; CURRENT APPLICATION NUMBER: US/10/311,455  
; CURRENT FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: PCT/EP01/07537  
; PRIOR FILING DATE: 2001-07-02  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 2424  
; SEQ ID NO 202  
; LENGTH: 6049  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-311-455-202

Query Match 37.7%; Score 219.8; DB 15; Length 6049;  
Best Local Similarity 70.0%; Pred. No. 2.9e-53;  
Matches 296; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 1 ATGGGACCCGACCTCGGCCCCAGACACAGGGGCTCTGTGTGACAGACTTTAGATTAT 60  
DB 1049 ATACGACCCCAACCTCGACCCCAACACAGAACTTAATAACAACCTTAATAATTAT 990  
QY 61 AAGCTGAGGAGAGGGTTATGTCTGTGAGCTGGCCCCCGGGAGGGGCCACAGACTGAC 120  
DB 989 AAACATAAACAATAAATATATATCTAATAAATAAACCAGAAAAAACCACAACTAAC 930  
QY 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCCGGCGCACC 180  
DB 929 CCGCTACACCAACCATACGAAACAATAAATAATTGAAACCCGCTTCCGACGACACC 870  
QY 181 TTCTCTGATCTGGGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 240  
DB 869 TTCTCTAATCTAAGCACTCACTACATATAAACCACCACTCAACCAACGCTTCACC 810  
QY 241 CAGGTCTCCGACGAATTTTCAAGGGGGCCCCAATGGGGCCGCTTGTAGCTTCTTT 300  
DB 809 CAATCTCCGATTAACCTTTTCAAAAAAACCACCACTAAACCGCTTATTAACCTTCTT 750  
QY 301 CTCTTTGGGGCTGCACTGTGTGTGAGAGTGTCAACAAGAGATGAACCACTGGTGGGA 360  
DB 749 ATCTTAATACTACATATATATAATAAATATCAACAAAAAATAAACCACCTAATAA 690  
QY 361 CAAGTGACAGAGTGTGATGTGGCTTACCTGAGACGCGGCTGTGACTGATCCACAGC 420  
DB 689 CAATATACAAATAAATAATTAACCTTAACCAACGCACTTAACCTAATAATCCACAAAC 630  
QY 421 AGT 423  
DB 629 AAT 627

RESULT 12

US-10-029-386-13384  
; Sequence 13384, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 13384  
; LENGTH: 590  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR14.3  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2  
; OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 2.00e-10  
; OTHER INFORMATION: NT HIT: g114751151, EVALUE 0.00e+00  
; OTHER INFORMATION: EST\_HUMAN HIT: AL157542.1, EVALUE 1.00e-119  
US-10-029-386-13384

Query Match 26.1%; Score 152; DB 16; Length 590;  
Best Local Similarity 100.0%; Pred. No. 8.3e-34;  
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 GCGGAGTTACAGCTCTATACGGGAGCGGGCCCTGAGAGAGCGCGCTGCGGGA 491  
Db 25 GCGGAGTTACAGCTCTATACGGGAGCGGGCCCTGAGAGAGCGCGCTGCGGGA 84  
QY 492 GGGGAAGTGGGATCAGTGAGGACAGTGTGACGGGGCCGTGCGACTGGGGCCCTGT 551  
Db 85 GGGGAAGTGGGATCAGTGAGGACAGTGTGACGGGGCCGTGCGACTGGGGCCCTGT 144  
QY 552 AACTGTAGGGGCTTTTGTCTAGCAAGTGA 583  
Db 145 AACTGTAGGGGCTTTTGTCTAGCAAGTGA 176

RESULT 13

US-10-029-386-27084  
; Sequence 27084, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 27084  
; LENGTH: 151  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR14.3  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2  
; OTHER INFORMATION: EST\_HUMAN HIT: AL157542.1, EVALUE 5.00e-70  
; OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 3.00e-11  
; OTHER INFORMATION: NT HIT: g114574571, EVALUE 9.00e-80

US-10-029-386-27084

Query Match 25.9%; Score 151; DB 16; Length 151;  
Best Local Similarity 100.0%; Pred. No. 1.4e-33;  
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 GCGGAGTTACAGCTCTATACGGGAGCGGGCCCTGAGAGAGCGCGCTGCGGGA 491  
Db 1 GCGGAGTTACAGCTCTATACGGGAGCGGGCCCTGAGAGAGCGCGCTGCGGGA 60  
QY 492 GGGGAAGTGGGATCAGTGAGGACAGTGTGACGGGGCCGTGCGACTGGGGCCCTGT 551  
Db 61 GGGGAAGTGGGATCAGTGAGGACAGTGTGACGGGGCCGTGCGACTGGGGCCCTGT 120  
QY 552 AACTGTAGGGGCTTTTGTCTAGCAAGTGA 582  
Db 121 AACTGTAGGGGCTTTTGTCTAGCAAGTGA 151

RESULT 14

US-09-864-761-17690  
; Sequence 17690, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aeomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 17690  
; LENGTH: 150



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 14:47:25 ; Search time 2841.37 Seconds  
(without alignments)  
7810.120 Million cell updates/sec

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Perfect score: 583  
Sequence: 1 atggcgaccagcagctcgcc.....cttttctagcaagtgaa 583

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_est2:  
3: gb\_hic:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_g881:  
9: gb\_g882:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	573.4	98.4	727	6	CD617893 56057475J
2	572.4	98.2	582	9	AY421020 Homo sapi
C 3	571.8	98.1	629	6	CD617891 56057367J
4	550	94.3	804	1	AL157542 DKFZp761D
5	548.4	94.1	1030	2	BE793530 60159016
6	526.4	90.3	643	7	CN281020 170005318
7	522.8	89.7	582	9	AY421022 Mus muscu
8	522.8	89.7	1949	3	AK015644 Mus muscu
9	522.8	89.7	3487	3	AK004680 Mus muscu
10	521.2	89.4	969	6	BY715200 BY715200
11	518.2	88.9	662	6	CD617892 56057475H
12	500	85.8	627	6	CD617890 56057367H
13	483.4	82.9	697	4	BI770566 603060362
14	465.6	79.9	967	5	BU503850 AGENCOURT
15	448	76.8	516	7	CN281015 170005321
16	443	76.0	626	6	CA391923 C820C09.Y
17	436	74.8	757	7	CK359685 AGENCOURT
18	434.2	74.5	713	5	BP753931 BP753931
19	423.2	72.6	583	5	BP355256 BP355256
20	423	72.6	583	5	BP249141 BP249141
21	421.4	72.3	584	5	BP311709 BP311709
22	417.6	71.6	643	4	BI910270 603069493
23	417	71.5	583	5	BP202031 BP202031
24	397	68.1	815	2	BF785386 602111728

25	381.8	65.5	623	6	CB578463	CB578463	AMGNNUC:N
26	375.4	64.4	854	3	AK013244	AK013244	Mus muscu
27	364.2	62.5	792	4	BG298789	BG298789	602396527
28	360	61.7	548	6	CA407899	CA407899	1004048 H
29	359	61.6	869	5	BU557268	BU557268	AGENCOURT
30	359	61.6	872	5	BU557410	BU557410	AGENCOURT
31	357.2	61.3	540	2	AW258810	um74a02.Y	
32	347.2	59.6	507	7	CN281011	328742965	
33	346.6	59.5	582	5	BP216712	BP216712	
34	340.2	58.4	752	7	CO401477	CO401477	AGENCOURT
35	332	56.9	437	6	CB790932	CB790932	AMGNNUC:N
36	331.2	56.8	440	6	CB749817	CB749817	AMGNNUC:M
37	330.8	56.7	630	7	CO040065	CO040065	UI-M-BH1-
38	326.8	56.1	758	4	BI764428	BI764428	603050701
39	317.8	54.5	1053	5	BU931540	BU931540	AGENCOURT
40	311.2	53.4	327	9	AY421021	AY421021	Pan trogl
41	305.2	52.3	559	6	BY704881	BY704881	BY704881
42	297.8	51.1	548	7	CF533813	CF533813	UI-M-FY0-
43	294.2	50.5	749	4	BG677345	BG677345	602624059
44	293.8	50.4	645	6	BY740551	BY740551	BY740551
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ALIGNMENTS

RESULT 1  
CD617893/c 727 bp mRNA linear EST 12-JAN-2004  
LOCUS 56057475J1 FLP Homo sapiens cDNA, mRNA sequence.  
DEFINITION CD617893  
ACCESSION CD617893  
VERSION CD617893.1 GI:40266158  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
TITLE 1 (bases 1 to 727)  
Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes

JOURNAL  
COMMENT Genomics 84 (1), 205-210 (2004)

CONTACT: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.

FEATURES  
Source location/Qualifiers  
1..727

/organism="Homo sapiens"  
/mol\_type="mRNA"  
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ORIGIN

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Best local similarity	99.0%	Pred. No. 2e-132		
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Db	608	ATGGCGACCCAGCCTCGGCCCCAGACACACGCGCTCTGTGGCAGACTTTGAGTTAT	549	
QY	61	AAGCTGAGGCGAAGAGGTTATGTCTGTGAGCTGCCCCGGGGAGGGCCCAAGCTGAC	120	
Db	548	AAGCTGAGGCGAAGAGGTTATGTCTGTGAGCTGCCCCGGGGAGGGCCCAAGCTGAC	489	
QY	121	CCGCTGACCAAGCATGCGGGCAGCTGAGATGATTGAGACCCGGCTTCGGCGCACC	180	
Db	488	CCGCTGACCAAGCATGCGGGCAGCTGAGATGATTGAGACCCGGCTTCGGCGCACC	429	
QY	181	TTCTCTGATCTGGCGGCTCAGCTGATGTAACCCAGGCTCAGCCCAAGCAAGCTTACC	240	

Db 428 TTCTCTGATCTGGCGGCTCAGCTCATGTGACCCAGGCTCAGCCCAACAGCTTCACC 369  
QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCCACTGGGGCCGCTTGTAGCCTTCTT 300  
Db 368 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCCCACTGGGGCCGCTTGTAGCCTTCTT 309  
QY 301 CTCTTTGGGGCTGCACTGTGTGCTGTAGAGTGTCAACAAGAGATGAACCACTGTGGGA 360  
Db 308 GTCTTTGGGGCTGCACTGTGTGCTGTAGAGTGTCAACAAGAGATGAACCACTGTGGGA 249  
QY 361 CAAGTCAGAGATGATGTGTGGCTTACCTTGAGACGCGGCTGTGACTGTGATCCACAGC 420  
Db 248 CAAGTCAGAGATGATGTGTGGCTTACCTTGAGACGCGGCTGTGACTGTGATCCACAGC 189  
QY 421 AGTGGGGGCTGGCGGAGTTCAACAGCTCTATACGGGGACGGGGCCCTGGAAGAGCGCGG 480  
Db 188 AGTGGGGGCTGGCGGAGTTCAACAGCTCTATACGGGGACGGGGCCCTGGAAGAGCGCGG 129  
QY 481 CGTCTGCGGAGGGGGAACCTGGCATCATGAGACAGAGTGTGACGGGGCCCTGGCACTG 540  
Db 128 CGTCTGCGGAGGGGGAACCTGGCATCATGAGACAGAGTGTGACGGGGCCCTGGCACTG 69  
QY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTGAA 583  
Db 68 GGGGCACCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTGAA 26

RESULT 2  
AY421020 582 bp DNA linear GSS 17-DEC-2003  
LOCUS Homo sapiens BCL2L2 gene, VIRTUAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AY421020 GI:39776977  
VERSION AY421020.1  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 582).  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 582)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence as made by sequencing genomic exons and ordering them  
based on alignment.  
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Location/Qualifiers  
1..582  
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/db\_xref="taxon:9606"  
<1..>582  
/gene="BCL2L2"  
/locus\_tag="HCM7418"

ORIGIN  
Query Match 98.2%; Score 572.4; DB 9; Length 582;  
Best Local Similarity 99.0%; Pred. No. 3.5e-132;  
Matches 576; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGGCAGCCCCAGCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGTTAT 60  
Db 1 ATGGCAGCCCCAGCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGTTAT 60  
QY 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGCCCCGGGAGGGCCCCAGCAGCTGAC 120  
Db 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGCCCCGGGAGGGCCCCAGCAGCTGAC 120  
QY 121 CCGCTGCACCAAGCCATGCGGGGAGAGATGAGTTGAGACCCGCTTCCGGCGCAC 180  
Db 121 CCACTGCACCAAGCCATGCGGGGAGAGATGAGTTGAGACCCGCTTCCGGCGCAC 180  
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAAGGCTCAGCCCAACGCTTCACC 240  
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QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCCACTGGGGCCCTTGTAGCCTTCTT 300  
Db 241 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCCCACTGGGGCCCTTGTAGCCTTCTT 300  
QY 301 CTCTTTGGGGCTGCACTGTGTGCTGTGAGTGTCAACAAGAGATGAACCACTGTGGGA 360  
Db 301 GTCTTTGGGGCTGCACTGTGTGCTGTGAGTGTCAACAAGAGATGAACCACTGTGGGA 360  
QY 361 CAAGTCAGAGATGATGTGTGGCTTACCTTGAGACGCGGCTGTGACTGATCCACAGC 420  
Db 361 CAAGTCAGAGATGATGTGTGGCTTACCTTGAGACGCGGCTGTGACTGATCCACAGC 420  
QY 421 AGTGGGGCTGGCGGAGTTCAACAGCTCTATACGGGGACGGGGCCCTGAGAGAGCGCGG 480  
Db 421 AGTGGGGCTGGCGGAGTTCAACAGCTCTATACGGGGACGGGGCCCTGAGAGAGCGCGG 480  
QY 481 CGTCTGCGGAGGGGGAACCTGGCATCATGAGACAGAGTGTGACGGGGCCCTGGCACTG 540  
Db 481 CGTCTGCGGAGGGGGAACCTGGCATCATGAGACAGAGTGTGACGGGGCCCTGGCACTG 540  
QY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTGAA 582  
Db 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTGAA 582

RESULT 3  
CD617891/c 629 bp mRNA linear EST 12-JAN-2004  
LOCUS CD617891  
DEFINITION 56057367J1 FLP Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD617891  
VERSION CD617891.1 GI:40266156  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 629)  
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
JOURNAL Genomics 84 (1), 205-210 (2004)  
CONTACT: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.

FEATURES  
Location/Qualifiers  
1..629  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="FLP"  
/note="Vector: pDrive Cloning Vector"

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Best Local Similarity 98.8%; Pred. No. 4.9e-132;

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Matches 576; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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Db 607 ATGGCGACCCAGCCTGGCCCCAGACACACGGGCTGTGTGGCAGACTTTAGGTTAT 548
QY 61 AAGCTGAGCAGAAAGGTTATGTGTGAGCTGCCCCGGGAGGCGCCAGCAGCTGAC 120
    |||||||
Db 547 AAGCTGAGCAGAAAGGTTATGTGTGAGCTGCCCCGGGAGGCGCCAGCAGCTGAC 488
QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTCCAGACCCGCTTCCGGCCACC 180
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Db 487 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTCCAGACCCGCTTCCGGCCACC 428
QY 181 TTCTCTGATCTGGGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 240
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Db 427 TTCTCTGATCTGGGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 368
QY 241 CAGGTCTCCAGCACTTTTCAAGGGGGCCCACTGGGGCCGCTTGTAGCCTTCTTT 300
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QY 301 CTCTTTGGGCTCACTGTGTGTGAGAGTCAACAAGAGATGAACCACTGGTGGGA 360
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QY 361 CAAGTGCAGAGTGGATGTGGCTACCTGAGACGCGGCTGTGACTGATCCACAGC 420
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Db 247 CAAGTGCAGAGTGGATGTGGCTACCTGAGACGCGGCTGTGACTGATCCACAGC 188
QY 421 AGTGGGGGCTGGGGGAGTTCAACAGCTCTATACGGGGACGGGGCCCTGGAGAGGCGCGG 480
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Db 187 AGTGGGGGCTGGGGGAGTTCAACAGCTCTATACGGGGACGGGGCCCTGGAGAGGCGCGG 128
QY 481 CGTCTGCGGAGGGGAAGTGGGATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540
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Db 127 CGTCTGCGGAGGGGAAGTGGGATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 68
QY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTGAA 583
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Db 67 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTGAA 25

RESULT 4
AL157542 804 bp mRNA linear EST 04-SEP-2003
LOCUS DKFP761D0816 r1 761 (synonym: hamy2) Homo sapiens cDNA clone
DEFINITION DKFP761D0816 5', mRNA sequence.
ACCESSION AL157542
VERSION AL157542
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 804)
AUTHORS Ansoerge,W., Wilkner,U., Mewes,W., Well,B. and Wiemann,S.
TITLE EST (Ansoerge,W., Wilkner,U., Mewes,H.W., Well,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFP761D0816) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY, Email: clone@rzpd.de.
FEATURES
Location/Qualifiers
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Best Local Similarity 98.6%; Pred. No. 1.4e-126;
Matches 575; Conservative 0; Mismatches 6; Indels 2; Gaps 2;
QY 1 ATGGCGACCCAGCCTGGCCCCAGACACAGGGCTGTGTGGCAGACTTTAGGTTAT 60
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Db 134 ATGGCGACCCAGCCTGGCCCCAGACACAGGGCTGTGTGGCAGACTTTAGGTTAT 193
QY 61 AAGCTGAGCAGAAAGGTTATGTGTGAGCTGCCCCGGGAGGCGCCAGCAGCTGAC 120
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QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTCCAGACCCGCTTCCGGCCACC 180
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Db 254 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTCCAGACCCGCTTCCGGCCACC 313
QY 181 TTCTCTGATCTGGGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 240
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Db 314 TTCTCTGATCTGGGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 373
QY 241 CAGGTCTCCAGCACTTTTCAAGGGGGCCCACTGGGGCCGCTTGTAGCCTTCTTT 300
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QY 301 CTCTTTGGGCTCACTGTGTGTGAGAGTCAACAAGAGATGAACCACTGGTGGGA 360
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QY 361 CAAGTGCAGAGTGGATGTGGCTACCTGAGACGCGGCTGTGACTGATCCACAGC 420
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Db 494 CAAGTGCAGAGTGGATGTGGCTACCTGAGACGCGGCTGTGACTGATCCACAGC 553
QY 421 AGTGGGGGCTGGGGGAGTTCAACAGCTCTATACGGGGACGGGGCCCTGGAGAGGCGCGG 480
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QY 481 CGTCTGCGGAGGGGAAGTGGGATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540
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QY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTGAA 583
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RESULT 5
BE793530 1030 bp mRNA linear EST 20-SEP-2000
LOCUS 601590016f1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944307 5',
DEFINITION mRNA sequence.
ACCESSION BE793530
VERSION BE793530
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1030)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
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COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-rt@mail.nih.gov  
Tissue Procurement: DCTD/DTP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium (LNL)  
Plate: LNCM800 row: p column: 04  
High quality sequence start: 5  
High quality sequence stop: 709.  
Location/Qualifiers  
1. 1030

FEATURES  
source

/organism="Homo sapiens"  
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/clone="IMAGE:3944307"  
/tissue\_type="small cell carcinoma"  
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/clone\_lib="NH\_MGC\_7"  
/note="Organ: Lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 94.1%; Score 548.4; DB 2; Length 1030;  
Best Local Similarity 96.4%; Pred. No. 3.7e-126;  
Matches 561; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
QY 1 ATGGCGACCCCAAGCTTGGCCCAAGACACACAGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
DB 144 ATGGCGACCCCAAGCTTGGCCCAAGACACACAGGGCTCTGGTGGCAGACTTTGTAGGTTAT 203  
QY 61 AAGCTGAGGCAAGGGTTATGTCTGTGAGAGCTGGCCCCGGGGAGGGCCCAAGAGCTGAC 120  
DB 204 AAGCTGAGGCAAGGGTTATGTCTGTGAGAGCTGGCCCCGGGGAGGGCCCAAGAGCTGAC 263  
QY 121 CCGCTGACCAAGCCATGCGGGCAGCTGGAGATGATGATGATGATGATGATGATGATGATGAT 180  
DB 264 CCACTGACCAAGCCATGCGGGCAGCTGGAGATGATGATGATGATGATGATGATGATGATGAT 323  
QY 181 TTCTGTGATCTGGCGGCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
DB 324 TTCTGTGATCTGGCGGCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 383  
QY 241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCACTGGGGCCGCTTGTAGCTTCTTT 300  
DB 384 CAGGTCTCCGATGAATTTTCAAGGGGGCCCACTGGGGCCGCTTGTAGCTTCTTT 443  
QY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAACTGATGATGATGATGAT 360  
DB 444 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAACTGATGATGATGATGAT 503  
QY 361 CAAGTCAGAGAGTGTGTGCTTACCTTGAGAGCGGGCTGTGCTGATGATGATGATGATGATGAT 420  
DB 504 CAAGTCAGAGAGTGTGTGCTTACCTTGAGAGCGGGCTGTGCTGATGATGATGATGATGATGAT 563  
QY 421 AGTGGGGCTGGGGGAGTTACAGCTCTTAACGGGGAGCGGGCCCTGGAGAGGCGGG 480  
DB 564 AGTGGGGCTGGGGGAGTTACAGCTCTTAACGGGGAGCGGGCCCTGGAGAGGCGGG 623  
QY 481 CGTCTCGGAGGGGAACTGGGCATCAGTGAAGACAGTGTGATCGGGGGCCGTGGCACTG 540  
DB 624 CGTCTCGGAGGGGAACTGGGCATCAGTGAAGACAGTGTGATCGGGGGCCGTGGCACTG 683  
QY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTAGCAAGTGA 582

Db

684 GGGGCTGGGTAACTGTAGGGGCTTTTGTAGCAAGTGA 725

RESULT 6  
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LOCUS 17000531876837 GRN\_EB Homo sapiens CDNA 5', mRNA sequence.  
DEFINITION CN281020  
ACCESSION CN281020  
VERSION CN281020.1 GI:47297434  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 643)  
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,  
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,  
Lebkowski,J and Stanton,L.W.  
Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
Nat. Biotechnol. 22 (6), 707-716 (2004)  
Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
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Location/Qualifiers  
1. 643

FEATURES  
source

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/note="oligo dT primed, full-length enriched cDNA library  
from embryoid body outgrowths derived from hES cell lines  
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free  
conditions."

ORIGIN

Query Match 90.3%; Score 526.4; DB 7; Length 643;  
Best Local Similarity 98.9%; Pred. No. 1.1e-120;  
Matches 530; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 ATGGCGACCCCAAGCTTGGCCCAAGACACACAGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
DB 108 ATGGCGACCCCAAGCTTGGCCCAAGACACACAGGGCTCTGGTGGCAGACTTTGTAGGTTAT 167  
QY 61 AAGCTGAGGCAAGGGTTATGTCTGTGAGAGCTGGCCCCGGGGAGGGCCCAAGAGCTGAC 120  
DB 168 AAGCTGAGGCAAGGGTTATGTCTGTGAGAGCTGGCCCCGGGGAGGGCCCAAGAGCTGAC 227  
QY 121 CCGCTGACCAAGCCATGCGGGCAGCTGGAGATGATGATGATGATGATGATGATGATGATGAT 180  
DB 228 CCGCTGACCAAGCCATGCGGGCAGCTGGAGATGATGATGATGATGATGATGATGATGATGAT 287  
QY 181 TTCTGTGATCTGGCGGCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
DB 288 TTCTGTGATCTGGCGGCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 347  
QY 241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCACTGGGGCCGCTTGTAGCTTCTTT 300  
DB 348 CAGGTCTCCGATGAATTTTCAAGGGGGCCCACTGGGGCCGCTTGTAGCTTCTTT 407  
QY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAACTGATGATGATGATGAT 360  
DB 408 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAACTGATGATGATGATGAT 467  
QY 361 CAAGTCAGAGAGTGTGTGCTTACCTTGAGAGCGGGCTGTGCTGATGATGATGATGATGATGAT 420



Db 468 CAAGTCAGAGTGGATGTGGCTTACCTGAGACGCGGCTGGCTGACTGGATCCACAGC 527

Qy 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGACGGGCGCTGGAGGAGCGCGG 480

Db 528 AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGAGCGGGCGCTGGAGGAGCGCGG 587

Qy 481 CGTCTGCGGAGGGGAAGTGGGATCAGTAGAGACAGTGTGACGGGGCGCTGGC 536

Db 588 CGTCTGCGGAGGGGAAGTGGGATCAGTAGAGACAGTGTGACGGGGCGCTGGC 643

RESULT 7  
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DEFINITION Mus musculus BCL2L2 gene, VIRTUAL TRANSCRIPT, partial sequence,  
AY421022  
ACCESSION AY421022  
VERSION AY421022.1  
KEYWORDS GI:39776979  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE  
AUTHORS Clark,A.G., Glanowski,S., Nielsen,R., Thomas,P., Kejarimal,A.,  
Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sniinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE  
AUTHORS Clark,A.G., Glanowski,S., Nielsen,R., Thomas,P., Kejarimal,A.,  
Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sniinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence as made by sequencing genomic exons and ordering them  
based on alignment.  
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Matches 545; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGTTAT 60  
Db 1 ATGGCGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

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Db 121 CCGCTGACCAAGCCATGCGGGCTGTGAGAGAGTTGAGACCCGCTTCGGCGCACC 180

Qy 181 TTCTCTGATCTGCGGCTCAGCTGATGTGACCCAGGCTCAGCCCAACGCTTCACC 240  
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Db 241 CAGTTTCCGACGAACCTTTTCCAGAGGGGCCCTAACTGGGGCGCTTGTGGCATTTCTT 300

Qy 301 CTCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAAGAGATGAAACCACTGTGGGA 360

Db 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCTTTGTGGGA 360

Qy 361 CAAGTCAGAGTGGATGTGTGGCCCTACCTGGAGACGGCGCTGTGACTGGATCCACAGC 420

Db 361 CAAGTCAGAGTGGATGTGTGGCCCTACCTGGAGACACAGTGTGCTGTGACTGGATCCACAGC 420

Qy 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGACGGGCGCTGGAGGAGCGCGG 480

Db 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGAGCGGGCGCTGGAGGAGCGCACGG 480

Qy 481 CGTCTGCGGAGGGGAAGTGGGATCAGTAGAGACAGTGTGACGGGGCGCTGGCACTG 540

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LOCUS 1949 bp mRNA linear HTC 03-APR-2004  
DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched  
library, clone:4930488D08 product:Bcl2-like 2, full insert  
sequence.  
ACCESSION AK015644  
VERSION AK015644.1  
KEYWORDS GI:12854052  
SOURCE HTC; CAP trapper.  
ORGANISM Mus musculus (house mouse)  
REFERENCE  
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
PUBMED 99279253  
REFERENCE  
AUTHORS Carninci,P. and Hayashizaki,Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
PUBMED 20499374  
REFERENCE  
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,  
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,  
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,  
Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,  
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,  
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861  
REFERENCE  
AUTHORS  
TITLE The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
JOURNAL Nature 409, 685-690 (2001)  
REFERENCE  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation



JOURNAL MEDLINE PUBMED	Genome Res. 10 (11), 1757-1771 (2000)
REFERENCE AUTHORS	20530913 11076861
TITLE JOURNAL REFERENCE AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
TITLE JOURNAL REFERENCE AUTHORS	5 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNA's Nature 420, 563-573 (2002)
TITLE JOURNAL REFERENCE AUTHORS	6 (bases 1 to 3487) Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE JOURNAL	Direct Submission Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	Please visit our web site ( <a href="http://genome.gsc.riken.jp/">http://genome.gsc.riken.jp/</a> ) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGCGCCGCACCTCGATTGTTTGTGTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence[5' GAGAGAGAAGGATCCAAGACTCAATTAAATTAATAACCCTCCCCC 3']. cDNA was cleaved with XhoI and SctI. Cloning sites, 5' end: SctI; 3' end: XhoI. Host: SOLR.
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Matches 545; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY       1 ATGGCGACCCAGCCTCGGCCGACACACAGGGCTGTGTGGCAGACTTTAGSTTAT 60
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QY       61 AAGCTGAGCGAGAAGGGTTATGTCTGTGAGCTGGCCCCGGGAGGGCCCAAGCTGAC 120
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QY       121 CCGCTGCACCAAGCCATGCGGSGAGCTGGAGATGAGTTGAGACCCCGCTTCGGGCGCAC 180
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QY       301 CTCTTTGGGGCTGCACACTGTGTCTGAGAGTGTCAAAGAGATGGAACCACTGTGTGGA 360
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QY       361 CAAGTGACAGAGTGGATGTGTGCTTACCCTGAGACCGGCTGTGCACTGGATCCACAGC 420
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Db        569 CAAGTGACAGAGTTGGATGTGTGCTTACCCTGAGACACGTTGTGCTGACTGATCCACAGC 628
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QY       421 AGTGGGGGCTGGGCGGAGTTTCAAGCTCTATACGGGGACGGGGCCCTGAGAGGCGCGG 480
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Db        629 AGTGGGGGCTGGGCGGAGTTTCAAGCTCTATACGGGGACGGGGCCCTGAGAGGCGCACGG 688
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QY       481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGGCGGTGGCACTG 540
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Db        689 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGGCGGTGGCACTG 748
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QY       541 GGGGCCCTGGTAAGTGTAGGGCCCTTTTTTGTCTAGCAAGTGA 582
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Db        749 GGGGCCCTGGTAAGTGTAGGGCCCTTTTTTGTCTAGCAAGTGA 790
         |||

RESULT 10
LOCUS      BY715200                      969 bp      mRNA      linear      EST 17-DEC-2002
DEFINITION BY715200 RIKEN full-length enriched, adult male testis Mus musculus
            CDNA clone 4930488D08 5', mRNA sequence.
ACCESSION  BY715200
VERSION     BY715200.1 GI:27128317
KEYWORDS   EST.
SOURCE      Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE 1
AUTHORS   Mammalyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
           1 (bases 1 to 969)
           Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
           Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
           Kiyoawara,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
           Schenbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bulc,C.,
           Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
           Batalov,S., Beisel,K.W., Blake,U.A., Bradt,D., Brusic,V.,
           Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
           Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
           Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,

```







Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.

FEATURES  
source  
1. .662  
Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="FLP"  
/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 88.9%; Score 518.2; DB 6; Length 662;  
Best Local Similarity 98.3%; Pred. No. 1.2e-118;  
Matches 534; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 ATGGCGACCCCAAGCTTCGGCCCCAGACACACGGGCTCTGTCGACAGCTTTGTAGTTAT 60  
DB 120 ATGGCGACCCCAAGCTTCGGCCCCAGACACACGGGCTCTGTCGACAGCTTTGTAGTTAT 179  
QY 61 AAGCTGAGGAGAGGGTTATGTCGTGAGCTGGCCCCGGGAGAGGCCAGAGAGCTGAC 120  
DB 180 AAGCTGAGGAGAGGGTTATGTCGTGAGCTGGCCCCGGGAGAGGCCAGAGAGCTGAC 239  
QY 121 CCGCTGCACCAAGCCATGCGGCGAGCTGAGATGAGTTGAGACCCGCTTCGGCGCACC 180  
DB 240 CCGCTGCACCAAGCCATGCGGCGAGCTGAGATGAGTTGAGACCCGCTTCGGCGCACC 299  
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAAGGCTCAGCCCAAGAGCTTCACC 240  
DB 300 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAAGGCTCAGCCCAAGAGCTTCACC 359  
QY 241 CAGGTCTCCGACGAATTTTCAAGGGGGCCCCCACTGGGGCCGCTTGAGCTTCTTT 300  
DB 360 CAGGTCTCCGATGAATTTTCAAGGGGGCCCCCACTGGGGCCGCTTGAGCTTCTTT 419  
QY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAAACAAGTGTGGGA 360  
DB 420 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAAACAAGTGTGGGA 479  
QY 361 CAAGTGACGAGTGA-TGGTGCCCTACCTGAGAGACGGGCTGTGCTGATCCACAG 419  
DB 480 CAAGTGACGAGTGA-TGGTGCCCTACCTGAGAGACGGGCTGTGCTGATCCACAG 539  
QY 420 CAGTGGGGGCTGGGGCGGAGTTCAAGCTCTATACGGGGACGGGCCCTGGAGAGGCGCG 479  
DB 540 CAGTGGGGGCTGGGGCGGAGTTCAAGCTCTATACGGGGACGGGCCCTGGAGAGGCGCG 599  
QY 480 GCGTCTGCGGAGGGGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACT 539  
DB 600 GCGTCTGCGGAGGGGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 659  
QY 540 GGG 542  
DB 660 GGG 662

RESULT 12  
LOCUS CD617890 627 bp mRNA linear EST 12-JAN-2004  
DEFINITION 56057367H1 FLP Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD617890  
VERSION CD617890.1 GI:40266155  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 627)  
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

JOURNAL Genomics 84 (1), 205-210 (2004)  
COMMENT Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.

FEATURES  
source  
1. .627  
Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone\_lib="FLP"  
/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 85.8%; Score 500; DB 6; Length 627;  
Best Local Similarity 99.0%; Pred. No. 4.2e-114;  
Matches 503; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCAAGCTTCGGCCCCAGACACACGGGCTCTGTCGACAGCTTTGTAGTTAT 60  
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QY 121 CCGCTGCACCAAGCCATGCGGCGAGCTGAGATGAGTTGAGACCCGCTTCGGCGCACC 180  
DB 240 CCGCTGCACCAAGCCATGCGGCGAGCTGAGATGAGTTGAGACCCGCTTCGGCGCACC 299  
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DB 300 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAAGGCTCAGCCCAAGAGCTTCACC 359  
QY 241 CAGGTCTCCGACGAATTTTCAAGGGGGCCCCCACTGGGGCCGCTTGAGCTTCTTT 300  
DB 360 CAGGTCTCCGATGAATTTTCAAGGGGGCCCCCACTGGGGCCGCTTGAGCTTCTTT 419  
QY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAAACAAGTGTGGGA 360  
DB 420 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAAACAAGTGTGGGA 479  
QY 361 CAAGTGACGAGTGA-TGGTGCCCTACCTGAGAGACGGGCTGTGCTGATCCACAGC 420  
DB 480 CAAGTGACGAGTGA-TGGTGCCCTACCTGAGAGACGGGCTGTGCTGATCCACAGC 539  
QY 421 AGTGGGGCTGGGGCGGAGTTCAAGCTCTATACGGGGACGGGCCCTGGAGAGGCGCGG 480  
DB 540 AGTGGGGCTGGGGCGGAGTTCAAGCTCTATACGGGGACGGGCCCTGGAGAGGCGCGG 599  
QY 481 CGTCTGCGGAGGGGAACTGGGCATCAG 508  
DB 600 CGTCTGCGGAGGGGAACTGGGCATCAG 627

RESULT 13  
LOCUS BI770566 697 bp mRNA linear EST 25-SEP-2001  
DEFINITION 603060362F1 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5209862 5', mRNA sequence.  
ACCESSION BI770566  
VERSION BI770566.1 GI:15762144  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 697)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
plate: LLAM1526 row: k column: 15  
High quality sequence start: 21  
High quality sequence stop: 695.  
Location/Qualifiers

FEATURES  
SOURCE

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/clone="IMAGE:5209862"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_122"  
/note="Organ: pooled lung and spleen. Vector: PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 82.9%; Score 483.4; DB 4; Length 697;  
Best Local Similarity 98.0%; Pred. No. 6e-110;  
Matches 542; Conservative 0; Mismatches 6; Indels 5; Gaps 5;

QY 1 ATGGCGACCCCGAGCTCGGCCCCAGACACACGGGCTGTGTGGCAGACTTTGTAGTTAT 60  
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QY 61 AAGCTGAGGCAGAAAGGTTATGTCTGTGAGCTGGCCCCGGGGAGGCCCCAGACTGAC 120  
Db 205 AAGCTGAGGCAGAAAGGTTATGTCTGTGAGCTGGCCCCGGGGAGGCCCCAGACTGAC 264  
QY 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCCGCTTCCGGCCGACC 180  
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QY 241 CAGGTCTCCGACGAATTTTCAAGGGGGCCCCCACTGGGGCCGCTTGTAGCTTCTTT 300  
Db 385 CAGGTCTCCGATGAATTTTCAAGGGGGCCCCCACTGGGGCCGCTTGTAGCTTCTTT 444  
QY 301 CTCTTTGGGGCTGCACTGTG-TGCTGAGAGTGTCAACAAGAGATGAAACAAGTGTGG 359  
Db 445 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAAACAAGTGTGG 504  
QY 360 ACAAGTGACGAGATGATGTTGCTGCTTACCT-GGAGACGGGGCCCTGGAGAGGCG 418  
Db 505 ACAAGTGACGAGATGATGTTGCTGCTTACCTGGAGAGACGGGGCCCTGGAGAGGCG 564  
QY 419 GCAGTGGGGCTGGGCGGAGTTCAAGCTTATAC-GGGAGCGGGCCCTGGAGAGGCG 477  
Db 565 GCAGTGGGGCTGGGCGGAGTTCAAGCTTATACGGGGAGCGGGCCCTGGAGAGGCG 624  
QY 478 CGGCGTCTGCGGAGGGGAAGTGGCA-TGAGTGAGACAG-TGCTGACGGGGCCGCTGG 535  
Db 625 CGGCGTCTGCGGAGGGGAAGTGGCAAGTGAAGACAGTTGCTGACGGGAGCCGCTGG 684  
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Db 685 CACTGGGGGCCCT 697

RESULT 14  
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DEFINITION  
AGENCOURT\_10030867 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:6491566  
5', mRNA sequence.  
BU503850  
BU503850.1 GI:22810083  
EST.  
Mus musculus (house mouse)  
Mus musculus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Unpublished (1999)  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM14043 row: c column: 23  
High quality sequence stop: 524.

FEATURES

SOURCE

1. 967  
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ORIGIN

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Best Local Similarity 92.5%; Pred. No. 1.8e-105;  
Matches 544; Conservative 0; Mismatches 39; Indels 5; Gaps 5;

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QY 241 CAGGTCTCCGACGAATTTTCAAGGGGGCCCCCACTGGGGCCGCTTGTAGCTTCTTT 300  
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QY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAAACCACTGGTGGGA 360  
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QY 361 CAAGTCAGAGAGTGGATGGTGGCCCTA-CCTGGAGACGGCGCTGTGCGACTGGATCCACAG 419  
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DB 490 CAAGTCAGAGATGGATGGTGGCCCTACCCCTGGAGACAGCTCTGGCTGACTGGATCCACAG 549  
QY 420 CAGT-GGGGGCTGGGGGAGTTCACAGCTCTATACGGGGAC-GGGGGCCCTGGAGGAGCG 477  
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DB 550 CAGTGGGGGCTGGGGGAGTTCACAGCTCTATACGGGGACGGGGGCCCTGGAGGAGCA 609  
QY 478 CGGCGTCTGCGGAGGGGAACTGGGCATCAGTGAAGACAGTGTCTGAC-GGGGGCCGTGGC 536  
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DB 610 CGGCGTCTGCGGAGGGGAACTGGGCATCAGTGAAGACAGTGTCTGACGGGGGCCGTGGC 669  
QY 537 ACTGGGGGCCCTGTAACTGT-AGGGGCTTTTGTCTAGCAAGTGA 583  
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LOCUS 17000532179318 GRN\_EB Homo sapiens cDNA 5', mRNA sequence.  
DEFINITION CN281015  
ACCESSION CN281015  
VERSION CN281015.1 GI:47297429  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS 1 (bases 1 to 516)  
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,  
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,  
Lebkowski, J. and Stanton, L.W.

TITLE Transcriptional characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)  
COMMENT Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
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FEATURES  
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H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free  
conditions."

ORIGIN

Query Match 76.8%; Score 448; DB 7; Length 516;  
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DB 121 AAGCTGAGGCAGAGGGTTATGTCTGTGAGCTGGCCCCGGGGGAGGGGCCAGACAGCTGAC 180  
QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCCGGCGCACC 180  
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DB 181 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCCGGCGCACC 240

QY 181 TTCTTGATCTGGCGGCTCAGCTGCATGTGACCCCAAGGCTCAGGCCAGACAGCTTCACC 240  
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DB 241 TTCTTGATCTGGCGGCTCAGCTGCATGTGACCCCAAGGCTCAGGCCAGACAGCTTCACC 300  
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QY 301 CTCTTGGGCTGCACTGTGTGCTGAGAGTCAACAAGAGATGAACCACTGTGGGA 360  
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DB 361 GTCTTGGGCTGCACTGTGTGCTGAGAGTCAACAAGAGATGAACCACTGTGGGA 420  
QY 361 CAAGTCAGAGATGGATGGTGGCCTACCTGAGACGGCGCTGGTGAAGTCCACAGC 420  
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DB 421 CAAGTCAGAGATGGATGGTGGCCTACCTGAGACGGCGCTGGTGAAGTCCACAGC 480  
QY 421 AGTGGGGCTGGCGCGAGTTCACAGCTTATACGGG 456  
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DB 481 AGTGGGGCTGGCGCGAGTTCACAGCTTATACGGG 516

Search completed: April 10, 2005, 20:12:29  
Job time : 2846.37 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2005, 22:21:58 ; Search time 19.5 Seconds  
(without alignments)  
738.834 Million cell updates/sec

Title: US-09-925-674B-7

Perfect score: 1007  
Sequence: 1 MATPASADPTRALVADFGVY.....LTGAVLALGALVTGAFPFASK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1007	100.0	193	4	US-09-155-327G-7
2	1007	100.0	193	4	US-09-949-016-10928
3	1002	99.5	193	1	US-08-798-897-4
4	1002	99.5	193	2	US-08-978-523-4
5	1000	99.3	193	4	US-09-155-327G-9
6	997	99.0	192	1	US-08-798-897-6
7	997	99.0	192	2	US-08-978-523-6
8	996	98.9	193	1	US-08-798-897-3
9	996	98.9	193	2	US-08-978-523-3
10	991	98.4	192	1	US-08-798-897-5
11	991	98.4	192	2	US-08-978-523-5
12	767	76.2	333	4	US-09-155-327G-10
13	766	76.1	365	4	US-09-149-476-696
14	766	76.1	365	4	US-09-010-147B-24
15	433.5	43.0	411	4	US-09-639-245-2
16	429.5	42.7	233	3	US-09-271-014A-6
17	428.5	42.6	233	1	US-08-333-565-59
18	428.5	42.6	233	1	US-08-081-448-6
19	428.5	42.6	233	1	US-08-607-269-24
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21	428.5	42.6	233	2	US-08-661-479-59
22	428.5	42.6	233	2	US-08-470-670A-7
23	428.5	42.6	233	3	US-08-471-057-14
24	428.5	42.6	233	3	US-08-481-739-2
25	428.5	42.6	233	3	US-09-167-921-2
26	428.5	42.6	233	3	US-09-323-743-2
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29	428.5	42.6	233	4	US-09-155-327G-12	Sequence 12, Appl
30	428.5	42.6	233	5	PCT-US94-07089-7	Sequence 7, Appl
31	428.5	42.6	233	5	PCT-US95-04600-24	Sequence 24, Appl
32	425	42.2	225	3	US-09-101-519-1	Sequence 1, Appl
33	423.5	42.1	233	1	US-08-607-269-23	Sequence 23, Appl
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35	413	41.0	236	1	US-08-607-269-22	Sequence 22, Appl
36	413	41.0	236	3	US-09-127-048-9	Sequence 9, Appl
37	413	41.0	236	5	PCT-US95-04600-22	Sequence 22, Appl
38	412.5	41.0	239	1	US-08-112-208C-10	Sequence 10, Appl
39	412.5	41.0	239	2	US-08-248-819A-10	Sequence 10, Appl
40	412.5	41.0	239	2	US-08-337-646A-10	Sequence 10, Appl
41	412.5	41.0	239	2	US-08-856-531-10	Sequence 10, Appl
42	412.5	41.0	239	2	US-08-856-034-10	Sequence 10, Appl
43	412.5	41.0	239	3	US-09-127-048-8	Sequence 8, Appl
44	412.5	41.0	239	3	US-08-927-326-10	Sequence 10, Appl
45	412.5	41.0	239	4	US-09-379-820A-10	Sequence 10, Appl

ALIGNMENTS

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RESULT 1
US-09-155-327G-7
; Sequence 7, Application US/09155327G
; Patent No. 6790637
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
; FILE REFERENCE: 2096584
; CURRENT APPLICATION NUMBER: US/09/155, 327G
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 193
; TYPE: PRT
; ORGANISM: HUMAN
US-09-155-327G-7

Query Match      100.0%; Score 1007; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 3.1e-107;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MATPASADPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQMRAAGDEFETRFRRT 60
DB      1 MATPASADPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQMRAAGDEFETRFRRT 60
QY      61 FSDLAOLHTVTPGSAQORFTQVSDDELFOGGPNMGRVLAFFVFGALCAESVNKEMEPLVG 120
DB      61 FSDLAOLHTVTPGSAQORFTQVSDDELFOGGPNMGRVLAFFVFGALCAESVNKEMEPLVG 120
QY      121 QVQEMWVAYLETRLADWIHSSGNAEFTALYGDGALBEARRLREGNWSVRTVLTGAVAL 180
DB      121 QVQEMWVAYLETRLADWIHSSGNAEFTALYGDGALBEARRLREGNWSVRTVLTGAVAL 180
QY      181 GALVTGAFPFASK 193
DB      181 GALVTGAFPFASK 193

RESULT 2
US-09-949-016-10928
; Sequence 10928, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
```

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; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10928
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10928

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Query Match          100.0%; Score 1007; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 3.1e-107;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MATPASAPDTRALVADFGVGYKLRQKGYCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60
Db 1 MATPASAPDTRALVADFGVGYKLRQKGYCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHVTTPGSAQQRFTQVSDELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120
Db 61 FSDLAQLHVTTPGSAQQRFTQVSDELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120
QY 121 QVQEMWVAYLETRLADWIHSSGMAEFTALYGDGALBEARRLREGNWSVRTLGAVAL 180
Db 121 QVQEMWVAYLETRLADWIHSSGMAEFTALYGDGALBEARRLREGNWSVRTLGAVAL 180
QY 181 GALVTVGAFPFASK 193
Db 181 GALVTVGAFPFASK 193

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```

RESULT 3
US-08-798-897-4
; Sequence 4, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids

```

```

; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-798-897-4

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```

Query Match          99.5%; Score 1002; DB 1; Length 193;
Best Local Similarity 99.5%; Pred. No. 1.2e-106;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MATPASAPDTRALVADFGVGYKLRQKGYCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60
Db 1 MATPASAPDTRALVADFGVGYKLRQKGYCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHVTTPGSAQQRFTQVSDELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120
Db 61 FSDLAQLHVTTPGSAQQRFTQVSDELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120
QY 121 QVQEMWVAYLETRLADWIHSSGMAEFTALYGDGALBEARRLREGNWSVRTLGAVAL 180
Db 121 QVQEMWVAYLETRLADWIHSSGMAEFTALYGDGALBEARRLREGNWSVRTLGAVAL 180
QY 181 GALVTVGAFPFASK 193
Db 181 GALVTVGAFPFASK 193

```

```

RESULT 4
US-08-978-523-4
; Sequence 4, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-978-523-4

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```

Query Match          99.5%; Score 1002; DB 2; Length 193;

```



APPLICATION NUMBER: US/08/978,523  
 FILING DATE: herewith  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/798,897  
 FILING DATE: February 11, 1997  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Esmond, Robert W.  
 REGISTRATION NUMBER: 32,893  
 REFERENCE/DOCKET NUMBER: 1483.0140002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 192 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-978-523-6

Query Match 99.0%; Score 997; DB 2; Length 192;  
 Best Local Similarity 99.5%; Pred. No. 4.3e-106;  
 Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 61  
 Db 1 ATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
 QY 62 SDLAALHTVTPGSAQORFTQVSDLEFQGGPNWGRVLVAFVFGAALCAESVNKEMEPLVG 121  
 Db 61 SDLAALHTVTPGSAQORFTQVSDLEFQGGPNWGRVLVAFVFGAALCAESVNKEMEPLVG 120  
 QY 122 VOEWNVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTVLTGAVALG 181  
 Db 121 VOEWNVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTVLTGAVALG 180  
 QY 182 ALVTVGAFPAASK 193  
 Db 181 ALVTVGAFPAASK 192

RESULT 8  
 US-08-798-897-3  
 Sequence 3, Application US/08798897  
 Patent No. 5789201  
 GENERAL INFORMATION:  
 APPLICANT: Guastella, John  
 TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
 TITLE OF INVENTION: Homologue  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 New York Avenue, N.W., Suite 600  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/798,897  
 FILING DATE: February 11, 1997  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Esmond, Robert W.  
 REGISTRATION NUMBER: 32,893  
 REFERENCE/DOCKET NUMBER: 1483.0140001

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 193 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-798-897-3

Query Match 98.9%; Score 996; DB 1; Length 193;  
 Best Local Similarity 98.4%; Pred. No. 5.7e-106;  
 Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
 Db 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
 QY 61 FSDLAALHTVTPGSAQORFTQVSDLEFQGGPNWGRVLVAFVFGAALCAESVNKEMEPLVG 120  
 Db 61 FSDLAALHTVTPGSAQORFTQVSDLEFQGGPNWGRVLVAFVFGAALCAESVNKEMEPLVG 120  
 QY 121 VOEWNVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTVLTGAVAL 180  
 Db 121 VOEWNVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTVLTGAVAL 180  
 QY 181 GALVTVGAFPAASK 193  
 Db 181 GALVTVGAFPAASK 193

RESULT 9  
 US-08-978-523-3  
 Sequence 3, Application US/08978523  
 Patent No. 583229  
 GENERAL INFORMATION:  
 APPLICANT: Guastella, John  
 TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
 TITLE OF INVENTION: Homologue  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 New York Avenue, N.W., Suite 600  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/978,523  
 FILING DATE: herewith  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/798,897  
 FILING DATE: February 11, 1997  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Esmond, Robert W.  
 REGISTRATION NUMBER: 32,893  
 REFERENCE/DOCKET NUMBER: 1483.0140002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 193 amino acids  
 TYPE: amino acid





Db 121 VQDMVTYLETRLADWIHSSGGMAEFTALYDGALEEARLRREGNWSVRTVLTGAVALG 180  
QY 182 ALVTGAFPAK 193  
Db 181 ALVTGAFPAK 192

RESULT 12  
US-09-155-327G-10  
; Sequence 10, Application US/09155327G  
; Patent No. 6790637  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2  
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES  
; FILE REFERENCE: 2096584  
; CURRENT APPLICATION NUMBER: US/09/155,327G  
; CURRENT FILING DATE: 1999-03-29  
; PRIOR APPLICATION NUMBER: PN8965  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 333  
; TYPE: PRT  
; ORGANISM: murine  
US-09-155-327G-10

Query Match 76.2%; Score 767; DB 4; Length 333;  
Best Local Similarity 74.4%; Pred. No. 2.2e-79;  
Matches 157; Conservative 6; Mismatches 18; Indels 30; Gaps 4;

QY 1 MATPASAPDTRALVADFGVYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
Db 1 MATPASPTDTRALVADFGVYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAQLHVTGPSAQQRFTQVSDELFOGGPNWGRVAFVFGAALCAESVNMKEMLVG 120  
Db 61 FSDLAQLHVTGPSAQQRFTQVSDELFOGGPNWGRVAFVFGAALCAESVNMKEMLVG 120  
QY 121 QVQEMWVAYLETRLADWIHSSGGMAEFTALYG--DGALEEARLR----- 164  
Db 121 QVQDMWVAYLETRLADWIHSSGGW-ELBAIKARVREMEEAELKELQNEVEKOMNMSP 179  
QY 165 -GN-----WASVRTVLTGAVALGA 182  
Db 180 PGNAGPVMSLEKMEADARSIVGNVDYGA 210

RESULT 13  
US-09-149-476-696  
; Sequence 696, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,336

; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,633  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,583  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,500  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,587  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,492  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,598  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,613  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,582  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,596  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,612  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,632  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,601  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,580  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,568  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,314  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,569  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,311  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,671  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,674  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,669  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,312  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,313  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,672  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,315  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/056,886  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,877  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,889  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,893  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,630  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,878  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,662  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,872  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,882  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,637  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,903  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,888  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,879  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,880  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,894  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,911  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,636  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,874  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,910  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,864  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,631  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,892  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,761  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047,595  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,599  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,588  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,585  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,586  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,590  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,594  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,589  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,593  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501

EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 76.1%; Score 766; DB 4; Length 365;  
Best Local Similarity 100.0%; Pred. No. 3.3e-79;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MATPASADTRALVADFGVYKLRQKGYVCGAGPGEPAADPLHQMRAAGDEFETRFRRT 60  
QY 61 FSDLAQHLHTPGSAQQRFTQVSDELFOGCPNMGRLVAFVFGAALCAESVNMKEPLVG 120  
DB 61 FSDLAQHLHTPGSAQQRFTQVSDELFOGCPNMGRLVAFVFGAALCAESVNMKEPLVG 120  
QY 121 QVQEWVAVYLETRLADWIHSSGGW 144  
DB 121 QVQEWVAVYLETRLADWIHSSGGW 144

RESULT 14  
US-09-010-147B-24

Sequence 24, Application US/09010147B  
Patent No. 6653445

GENERAL INFORMATION:

APPLICANT: Nl et al.

TITLE OF INVENTION: Human Proteins

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC

compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,147B  
FILING DATE: 12-Jan. 6653445-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,205  
FILING DATE: 21-JAN-1997  
APPLICATION NUMBER: US 60/034,204  
FILING DATE: 21-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Jonathan L. Klein  
REGISTRATION NUMBER: 41,119  
REFERENCE/DOCKET NUMBER: PF353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 365 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
US-09-010-147B-24

Query Match 76.1%; Score 766; DB 4; Length 365;  
Best Local Similarity 100.0%; Pred. No. 3.3e-79;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRRRT 60  
DB 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRRRT 60  
QY 61 FSDLAQLHVTGPSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVKNKEMEPVVG 120  
DB 61 FSDLAQLHVTGPSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVKNKEMEPVVG 120  
QY 121 QVQEMWVAYLETRLADWIHSSGGW 144  
DB 121 QVQEMWVAYLETRLADWIHSSGGW 144

RESULT 15  
US-09-639-245-2  
Sequence 2, Application US/09639245  
Patent No. 6737511  
GENERAL INFORMATION:  
APPLICANT: Youle et al.  
TITLE OF INVENTION: RECEPTOR-MEDIATED UPTAKE OF AN EXTRACELLULAR BCL-XL  
TITLE OF INVENTION: FUSION PROTEIN INHIBITS APOPTOSIS  
FILE REFERENCE: 4239-55417  
CURRENT APPLICATION NUMBER: US/09/639,245  
CURRENT FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: 60/149,220  
PRIOR FILING DATE: 1999-08-16  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 411  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: genetic fusion  
US-09-639-245-2

Query Match 43.0%; Score 433.5; DB 4; Length 411;  
Best Local Similarity 39.9%; Pred. No. 5.2e-41;  
Matches 93; Conservative 26; Mismatches 63; Indels 51; Gaps 4;

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QY 40 D-----PLHQAMRAAGDEFETRRRTFSDLAQLHVTGPSAQORFTQ 81

DB 86 NGATAHSSSLDAREVTPMAAVKQALREAGDEFELRYRAFSDLTSQHLITPGTAYQSFEQ 145  
QY 82 VSDELFQGGPNWGRLVAFVFGAALCAESVKNKEMEPVVGQVQEMWVAYLETRLADWIHSS 141  
DB 146 VVNEIFRDGVNWGRIVAFSFGALCVESVDKEMQVLSRIAAMMATYLNHLEPWIQEN 205  
QY 142 GGWAFTALYGDGALLEARRIRE--GNWASVRTVLTGAVAGALVTGAFAS 192  
DB 206 GGWDTFVELYGNNAAESRKQGERFNRWFLTGMTVAGVVLIGSLFSRKAYSAA 258

Search completed: April 10, 2005, 22:45:27  
Job time : 21.5 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 10, 2005, 20:17:32 ; Search time 59 Seconds  
(without alignment)  
1675.106 Million cell updates/sec

Title: US-09-925-674B-7  
Perfect score: 1007  
Sequence: 1 MATPASAPDTRALVADFGVY.....LTGAVALGALVTGAFPAASK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1007	100.0	193	1 BCLW_HUMAN	Q92843 homo sapien
2	1000	99.3	193	1 BCLW_MOUSE	P70345 mus musculu
3	996	98.9	193	2 O88996	O88996 rattus norv
4	996	98.9	219	2 Q7TS60	Q7TS60 rattus norv
5	987	98.0	192	2 Q6A093	Q6A093 mus musculu
6	951	94.4	193	2 Q8CG14	Q8CG14 mus musculu
7	761	75.6	178	2 Q8CFR2	Q8CFR2 mus musculu
8	761	75.6	178	2 Q9CYW5	Q9CYW5 mus musculu
9	651.5	64.7	188	2 Q6GP82	Q6GP82 xenopus lae
10	646.5	64.2	228	1 ARL_XENLA	Q91827 xenopus lae
11	440.5	43.7	233	2 Q9MYW4	Q9MYW4 oryctolagus
12	433.5	43.0	233	2 Q8SQ42	Q8SQ42 felis silve
13	432.5	42.9	229	1 BCLX_CHICK	Q07816 gallus gall
14	431.5	42.9	233	1 BCLX_PIG	Q77737 sus scrofa
15	431.5	42.9	233	2 Q9N1A2	Q9N1A2 sus scrofa
16	428.5	42.6	233	1 BCLX_HUMAN	Q07817 homo sapien
17	428.5	42.6	233	1 BCLX_MOUSE	Q64373 mus musculu
18	428.5	42.6	233	1 BCLX_RAT	P53563 rattus norv
19	428.5	42.6	233	2 Q76LT7	Q76LT7 canis fami
20	428.5	42.6	233	2 Q9MZS7	Q9MZS7 ovis aries
21	423.5	42.1	233	1 BCL2_CHICK	Q00709 gallus gall
22	416.5	41.4	229	1 BCL2_BOVIN	Q02718 bos taurus
23	414	41.1	236	1 BCL2_RAT	P49950 rattus norv
24	413	41.0	236	1 BCL2_MOUSE	P10417 mus musculu
25	413	41.0	236	2 Q7TSN8	Q7TSN8 rattus norv
26	413	41.0	236	2 Q8BQK4	Q8BQK4 mus musculu
27	412.5	41.0	239	1 BCL2_HUMAN	P10415 homo sapien
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29	403	40.0	238	2 Q90Z98	Q90Z98 brachydanio
30	402.5	40.0	239	2 Q75SV7	Q75SV7 canis fami
31	402	39.9	79	2 Q7TS61	Q7TS61 rattus norv

32	401	39.8	180	2 Q9BDD5	Q9bdd5 bos taurus
33	401	39.8	217	2 Q99N35	Q99n35 mus musculu
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36	398.5	39.6	201	2 Q6GLI5	Q6gli5 xenopus tro
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38	396	39.3	236	2 Q6R755	Q6r755 canis fami
39	380.5	37.8	284	2 Q7TS62	Q7TS62 rattus norv
40	374.5	37.2	188	2 Q9QWX2	Q9qwx2 mus musculu
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44	371	36.8	204	1 ARL1_XENLA	Q91828 xenopus lae
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ALIGNMENTS

RESULT 1  
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ID BCLW\_HUMAN STANDARD; PRT; 193 AA.  
AC Q92843;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Apoptosis regulator Bcl-w (Bcl-2-like 2 protein).  
GN Name=BCL2L2; Synonyms=BCLW, KIAA0271;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
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RP SEQUENCE FROM N.A.  
RX MEDLINE=96358615; PubMed=8761287;  
RA Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,  
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.,  
RT "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";  
RL Oncogene 13:665-675(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=97191544; PubMed=9039502;  
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,  
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.,  
RT "Prediction of the coding sequences of unidentified human genes. VI.  
RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by  
RT analysis of cDNA clones from cell line KG-1 and brain.";  
RL DNA Res. 3:321-329(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzywicki M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

```

CC -1- FUNCTION: Promotes cell survival.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and
CC in a wide range of tissues, with highest levels in brain, colon,
CC and salivary gland.
CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC function.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U59747; AAB09055.1; -.
CC EMBL; D87461; BAA19666.2; ALT_INIT.
CC EMBL; BC021198; AAH21198.1; -.
CC PDB; 1MK3; NMR; A=2-172.
CC PDB; 100L; NMR; A=1-183.
CC Genew; HGNC:995; BCL2L2.
CC H-INVD; HIX0011536; -.
CC MIM; 601931; -.
CC DR GO; GO:005737; C:cytoplasm; NAS.
CC DR GO; GO:0006916; P:anti-apoptosis; TAS.
CC DR GO; GO:007283; P:spermatogenesis; TAS.
CC DR InterPro; IPR00712; Bcl2_BH.
CC DR InterPro; IPR03093; Bcl2_BH4.
CC DR InterPro; IPR02475; BCL2_family.
CC DR Pfam; PF00452; Bcl-2; 1.
CC DR Pfam; PF02180; BH4; 1.
CC DR PROSITE; PS50062; BCL2_FAMILY; 1.
CC DR PROSITE; PS01080; BH1; 1.
CC DR PROSITE; PS01258; BH2; 1.
CC DR PROSITE; PS01260; BH4_1; 1.
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CC DR PROSITE; PS50063; BH4_2; 1.
CC DR 3D-structure; Apoptosis.
CC FT DOMAIN 9 29 BH4.
CC FT DOMAIN 85 104 BH1.
CC FT DOMAIN 136 151 BH2.
CC SQ SEQUENCE 193 AA; 20774 MW; 3792243A50281761 CRC64;

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Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 FSDLAQLHVTPEGAQQRFTQVSDLELFGGPNWGRLVAFVFGAALCAESVKNKEMEPLVG 120
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QY 181 GALVTGAFPAASK 193
DB 181 GALVTGAFPAASK 193

RESULT 2
BCLW_MOUSE STANDARD; PRT; 193 AA.
AC P70345;
DT 01-NOV-1997 (Rel. 35, Created)

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DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Apoptosis regulator Bcl-w (Bcl-2-like 2 protein).
GN Name=Bcl2l2; Synonyms=Bclw;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358615; PubMed=8761287;
RA Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;
RT "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
RL Oncogene 13:665-675(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/10J;
RX MEDLINE=98160183; PubMed=9500547;
RA Ross A.J., Waymire K.G., Moss J.E., Parlow A.F., Skinner M.K.,
RA Russell L.D., Macgregor G.R.;
RT "Testicular degeneration in Bclw-deficient mice.";
RL Nat. Genet. 18:251-256(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamana H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
CC -1- FUNCTION: Promotes cell survival.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and
CC in a wide range of tissues, with highest levels in brain, colon,
CC and salivary gland.
CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC function.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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RESULT 4  
Q7TS60  
ID Q7TS60 PRELIMINARY; PRT; 219 AA.  
AC Q7TS60;  
DT 01-OCT-2003 (TREMBlrel. 25, Created)  
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE BCL-WEL.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=22672518; PubMed=12787069;  
RA Itoh T., Itoh A., Pleasure D.;  
RT "Bcl-2-related protein family gene expression during oligodendroglial  
RT differentiation.";  
RL J. Neurochem. 85:1500-1512(2003).  
DR EMBL; AY185100; AA064470.1; -.  
DR HSSP; Q07817; 1R2D.  
DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
DR InterPro; IPR00712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; Bcl2\_family.  
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DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
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DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
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Best Local Similarity 98.4%; Pred. No. 4.8e-81;  
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEGPADPLHQAMRAAGDEFETRFRRT 60  
DB 27 MATPASTPDRALVADFGVGYKLRQKGYVCGAGPGEGPADPLHQAMRAAGDEFETRFRRT 86  
QY 61 FSDLAQLHVTGPSAQQRFTQVSDELFGGGPNWGRVAFVFGAALCAESVKNKEMEPLVG 120  
DB 87 FSDLAQLHVTGPSAQQRFTQVSDELFGGGPNWGRVAFVFGAALCAESVKNKEMEPLVG 146  
QY 121 QVQEMWVAYLETRLADWIHSSGGWAEFTALYGDGALLEEARRLREGNWASVRTVLTGAVAL 180  
DB 147 QVQDMWVYLETRLADWIHSSGGWAEFTALYGDGALLEEARRLREGNWASVRTVLTGAVAL 206  
QY 181 GALVTVGAFPAK 193  
DB 207 GALVTVGAFPAK 219  
RESULT 5  
Q6A093  
ID Q6A093 PRELIMINARY; PRT; 192 AA.  
AC Q6A093;  
DT 25-OCT-2004 (TREMBlrel. 28, Created)  
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE KIAA0271 protein (Fragment).  
GN Name=KIAA0271;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,  
RA Saza Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,  
RA Nagase T., Ohara O., Koga H.;  
RT "Prediction of the Coding Sequences of Mouse Homologues of KIA Gene:  
RT IV. The Complete Nucleotide Sequences of 500 Mouse KIA-Homologous  
RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones  
RT Randomly Sampled from Size-Fractionated Libraries.";  
RL DNA Res. 11:205-218(2004).  
DR EMBL; AK172925; BAD32203.1; -.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0005515; F:protein binding; IPT.  
DR GO; GO:0006915; P:apoptosis; IDA.  
DR InterPro; IPR00712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; Bcl2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
FT NON TER 1  
SQ SEQUENCE 192 AA; 20763 MW; A56CE4EC51D41F8A CRC64;  
Query Match 98.0%; Score 987; DB 2; Length 192;  
Best Local Similarity 98.9%; Pred. No. 2.6e-80;  
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEGPADPLHQAMRAAGDEFETRFRRT 60  
DB 2 MATPASTPDRALVADFGVGYKLRQKGYVCGAGPGEGPADPLHQAMRAAGDEFETRFRRT 61  
QY 61 FSDLAQLHVTGPSAQQRFTQVSDELFGGGPNWGRVAFVFGAALCAESVKNKEMEPLVG 120  
DB 62 FSDLAQLHVTGPSAQQRFTQVSDELFGGGPNWGRVAFVFGAALCAESVKNKEMEPLVG 121  
QY 121 QVQEMWVAYLETRLADWIHSSGGWAEFTALYGDGALLEEARRLREGNWASVRTVLTGAVAL 180  
DB 122 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALLEEARRLREGNWASVRTVLTGAVAL 181  
QY 181 GALVTVGAF 190  
DB 182 GALVTVGAF 191  
RESULT 6  
Q8CGL4  
ID Q8CGL4 PRELIMINARY; PRT; 193 AA.  
AC Q8CGL4;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Bcl2-like protein 2.  
GN Name=Bcl2l2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL; TISSUE=Skin;  
RA Su H.-Y., Cheng W.T.K., Chen S.C., Lin C.T., Lien Y.Y., Liu H.J.,  
RA Gilmore R.S.;  
RT "Mouse keratinocytes express c98, a novel gene homologous to bcl-2,  
RT that is stimulated by insulin-like growth factor 1 and prevents  
RT dexamethasone-induced apoptosis.";  
RL Biochim. Biophys. Acta 1676:127-137(2004).  
DR EMBL; AY170344; AA013177.2; -.  
DR HSSP; Q92843; 100L.  
DR MGD; MGI:108052; Bcl2l2.



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DR GO; GO:0016021; C:Integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPT.
DR GO; GO:0006915; P:apoptosis; IDA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
SQ SEQUENCE 193 AA; 20958 MW; 60D7F9E4DC56DFAE CRC64;

Query Match          94.4%; Score 951; DB 2; Length 193;
Best Local Similarity 94.8%; Pred. No. 4.4e-77;
Matches 183; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60
DB 1 MATPASTPDTRALVAYFVGYYQLRQKGYVCGAGPEGPAADPLHQAMRAAGDELQTRFRRT 60
QY 61 FSDLAQLHTVTPGSAQQRFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNMKEPVLVG 120
DB 61 FSHLAAQLHTVTPGSAQQRFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNMKEPVLVG 120
QY 121 QVQEMWVAYLETRLADWIIHSSGGWAEFTALYGDGALIEARRLREGNWASVTVLTGAVAL 180
DB 121 QVQDMWVAYLETRLAYWIHSSGGWAEFTALYGDGALIEARRLREGNWASVTVLTGAVAL 180
QY 181 GALVTVGAFPAK 193
DB 181 GALVTVGAFPAK 193
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RESULT 7
Q8CFR2 PRELIMINARY; PRT; 178 AA.
AC Q8CFR2;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Bcl2l2 protein.
GN Name=Bcl2l2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kesteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
RA Krzywinski M.I., Skalek U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
```

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RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC040369; AAH40369.1; -.
DR HSSP; Q92843; 100L.
DR MGD; MGI:108052; Bcl2l2.
DR GO; GO:0016021; C:Integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPT.
DR GO; GO:0006915; P:apoptosis; IDA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 178 AA; 19119 MW; E2C3F3F79528E9D7 CRC64;

Query Match          75.6%; Score 761; DB 2; Length 178;
Best Local Similarity 95.3%; Pred. No. 4.1e-60;
Matches 143; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60
DB 1 MATPASTPDTRALVAYFVGYYQLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHTVTPGSAQQRFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNMKEPVLVG 120
DB 61 FSDLAQLHTVTPGSAQQRFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNMKEPVLVG 120
QY 121 QVQEMWVAYLETRLADWIIHSSGGWAEFTAL 150
DB 121 QVQDMWVAYLETRLADWIIHSSGGWVRSSQL 150
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RESULT 8
Q9CYW5 PRELIMINARY; PRT; 178 AA.
AC Q9CYW5;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2810435A13 product:Bcl2-like 2, full insert
DE sequence.
GN Name=Bcl2l2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=whole body;
```

RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630 (2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771 (2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK013244; BAB28740.1; -.  
DR HSSP; Q92843; 100L.  
DR MGD; MGI:108052; Bcl2l2.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0006915; P:apoptosis; IDA.  
DR InterPro; IPR003093; Bcl2\_BH.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR002475; Bcl2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
SQ SEQUENCE 178 AA; 19147 MW; E2D4C3F79528E9D7 CRC64;  
Query Match 75.6%; Score 761; DB 2; Length 178;  
Best Local Similarity 95.3%; Pred. No. 4.1e-60;  
Matches 143; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASTPDRALVADFVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDIAAQLHVTGPSAQORFTQVSDLELFGGPNWGRVLVAFVFGAALCAESVKNKEMEPLVG 120  
DB 61 FSDIAAQLHVTGPSAQORFTQVSDLELFGGPNWGRVLVAFVFGAALCAESVKNKEMEPLVG 120

QY 121 QVQEWVAYLETRLADWIHSSGGWAEFTAL 150  
DB 121 QVQDMVAYLETRLADWIHSSGGWVRSSQL 150  
RESULT 9  
Q6GP82 PRELIMINARY; PRT; 188 AA.  
AC Q6GP82;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE MGC80617 protein.  
GN Name=MGC80617;  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshlyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Shevchenko Y., Bouffard G.G.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative.";  
RL Dev. Dyn. 225:384-391 (2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Klein S., Gerhard D.S.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073259; AAH73259.1; -.  
DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH.  
DR InterPro; IPR002475; Bcl2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
SQ SEQUENCE 188 AA; 20441 MW; CB3C1A8C55F16B96 CRC64;  
Query Match 64.7%; Score 651.5; DB 2; Length 188;

Best Local Similarity 68.9%; Pred. No. 2.8e-50;  
Matches 126; Conservative 20; Mismatches 34; Indels 3; Gaps 1;

QY 11 RALVADPVGYKLRQKGYVCAGPGEPPADPLHQAMRAAGDEFETRFRRTFSDLAQLH 70  
Db 9 RALVEDFVRYYKLCQSLV--PEPAGPASCALHSAMRAAGDEFEEFRQAIFSEISTQIH 65  
QY 71 TPGSAOQRFQVSDLEFQGGPNMGRVLVAFVFGAALCAESVNKEMEPLVGQVQEMVAYL 130  
Db 66 TPGTAYARFAEVAAGSLFQGGVNMGRIVAFVFGAALCAESVNKEMSPLLPRIQDMWVTVL 125  
QY 131 ETRLADWIHSSGWAFFLTALYGDGALIEARRLRREGNMAVSVTVLTGAVAGALVTGAF 190  
Db 126 ETNLRGWIQSNGWNGFLLTYGDGALIEARRQREGNMAVSLKTVLTGAVAGALMTVGALF 185  
QY 191 ASK 193  
Db 186 ASK 188

RESULT 10

ARI\_XENLA STANDARD; PRT; 228 AA.  
ID ARI\_XENLA  
AC Q91827;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 29-MAR-2004 (Rel. 43, Last annotation update)  
DE Apoptosis regulator R1 (XR1) (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Head;  
RX MEDLINE=95331613; PubMed=7607538; DOI=10.1016/0378-1119(95)00159-4;  
RA Cruz-Reyes J., Tata J.R.;  
RT "Cloning, characterization and expression of two Xenopus bcl-2-like  
RT cell-survival genes.";  
RL Gene 158:171-179(1995).  
CC -1- FUNCTION: Could be the homolog of mammalian Bcl-W.  
CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).  
CC -1- DEVELOPMENTAL STAGE: Developmental regulation only occurs in the  
CC brain of mid-metamorphic to post-metamorphic tadpoles and  
CC adults, where an increase of several fold has been observed.  
CC -1- SIMILARITY: Belongs to the Bcl-2 family.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL; X82462; CAA57845.1; -.  
DR HSSP; Q07817; IMAZ.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; Bcl2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR Apoptosis; Transmembrane.  
FT NON\_TER 1 1  
FT DOMAIN 120 139 BH1.  
FT DOMAIN 171 186 BH2.  
FT TRANSMEM 207 227 Potential.

SQ SEQUENCE 228 AA; 25068 MW; C499D449A585F8A9 CRC64;

Query Match 64.2%; Score 646.5; DB 1; Length 228;  
Best Local Similarity 67.9%; Pred. No. 9.6e-50;  
Matches 125; Conservative 21; Mismatches 35; Indels 3; Gaps 1;

QY 10 TRALVADPVGYKLRQKGYVCAGPGEPPADPLHQAMRAAGDEFETRFRRTFSDLAQLH 69  
Db 48 SRALVEDLVRYKLCQSLV--PEPSGAASCALHSAMRAAGDEFEEFRQAIFSEISTQIH 104  
QY 70 VTPGSAOQRFQVSDLEFQGGPNMGRVLVAFVFGAALCAESVNKEMEPLVGQVQEMVAY 129  
Db 105 VTPGTAYARFAEVAAGSLFQGGVNMGRIVAFVFGAALCAESVNKEMSPLLPRIQDMWVTV 164  
QY 130 LETRLADWIHSSGWAFFLTALYGDGALIEARRLRREGNMAVSVTVLTGAVAGALVTGAF 189  
Db 165 LETNLRDWIQSNGWNGFLLTYGDGALIEARRQREGNMAVSLKTVLTGAVAGALMTVGAL 224  
QY 190 FASK 193  
Db 225 FASK 228

RESULT 11

Q9MYW4 PRELIMINARY; PRT; 233 AA.  
ID Q9MYW4  
AC Q9MYW4;  
DT 01-OCT-2000 (TRENBLREL. 15, Created)  
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)  
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)  
DE Bcl-X.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Knott J.C., Robertson L., James E.R.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY005131; AAF88137.1; -.  
DR HSSP; P53563; 1AF3.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
SQ SEQUENCE 233 AA; 25986 MW; 12F0F30344D53F93 CRC64;

Query Match 43.7%; Score 440.5; DB 2; Length 233;  
Best Local Similarity 42.0%; Pred. No. 2.7e-31;  
Matches 94; Conservative 22; Mismatches 57; Indels 51; Gaps 4;

QY 11 RALVADPVGYKLRQKGYVC-----GAG-----PGEPPAA 39  
Db 6 RELVVDPLSYKLSQKYSWSQFSDVENRTEAPEGTGPEMETPSAINGNPAMHPADSPAV 65  
QY 40 D-----PLHQAMRAAGDEFETRFRRTFSDLAQLHVTGSAOQRFQ 81  
Db 66 NGATGHSSSLDAREVTPMTAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125  
QY 82 VSDELFGGPNMGRVLVAFVFGAALCAESVNKEMEPLVGQVQEMVAYLETRLADWIHSS 141

Db 126 VVNELFRDGVNMGRIVAFPSFGALCVESVDKEMEVLSRIAAMMATYLNHLEPWIQEN 185  
Qy 142 GGWAEFTALYGDGALIEEARLRE--GNWASVRTVLTGAVLGAAL 183  
Db 186 GGWDTFVELYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSL 229

## RESULT 12

Q8SQ42 PRELIMINARY; PRT; 233 AA.  
AC Q8SQ42;  
DT 01-JUN-2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE Bcl-x1 protein.  
GN Name=bcl-x1;  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Nagafuchi S., Sano J., Kano R., Hasegawa A.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB080951; BAB85856.2; -.  
DR HSSP; Q07817; IMAZ.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
SQ SEQUENCE 233 AA; 26017 MW; CD17F24FE9D47BC9 CRC64;

Query Match 43.0%; Score 433.5; DB 2; Length 233;  
Best Local Similarity 41.6%; Pred.No.1.1e-30;  
Matches 97; Conservative 23; Mismatches 58; Indels 55; Gaps 5;

Qy 11 RALVADFVGYKLRQKY-----V 28  
Db 6 RELVDFLSYKLSQGYSWSRFSVDVENRTAEPTGESEMETPSAINGNPSWHLADSPAV 65  
Qy 29 CGAGPGEPPAD-----PLHOAMRAAGDEFETRRRTFSDLAQLHVTGSAQQRFT 80  
Db 66 NGA-TGHSSSLDAREVTPMAAVKQALREAGDEFELRYRAFSDLTSQLHTPGTAYQSFE 124  
Qy 81 QVSDLFQGGPNWGRVAVFVFGAALCAESVKNKEMBLVGQVQEMWVAVLETRLDWIHS 140  
Db 125 QVVNELFRDGVNMGRIVAFPSFGALCVESVDKEMQVLSRIAAMMATYLNHLEPWIQ 184  
Qy 141 SGGWAEFTALYGDGALIEEARRLREGNWSVRTVLTGAVLGAALVTGAFPAK 193  
Db 185 NGGWDTFVELYGNNAAESRK--GQERSNRWFLTGMTVAG-VLLGSLFSRK 233

RESULT 13  
BCLX\_CHICK STANDARD; PRT; 229 AA.  
AC Q07816; Q98908;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).  
GN Name=BCL2L1; Synonyms=BCL-X, BCLX;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
RX MEDLINE=93364977; PubMed=8358789; DOI=10.1016/0092-8674(93)90508-N;  
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,  
RA Turka L.A., Mao X., Nunez G., Thompson C.B.;  
RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator of  
RT apoptotic cell death."  
RL Cell 74:597-608(1993).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM LONG).  
RC STRAIN=Hubbard White Mountain; TISSUE=Testis;  
RX MEDLINE=97264485; PubMed=9110311;  
RX DOI=10.1002/(SICI)1098-2795(199705)47:1<26::AID-MRD4>3.3.CO;2-V;  
RA Vilagrasa X., Mezquita C., Mezquita J.;  
RT "differential expression of bcl-2 and bcl-x during chicken  
RT spermatogenesis."  
RL Mol. Reprod. Dev. 47:26-29(1997).  
CC -1- FUNCTION: Dominant regulator of apoptotic cell death. The long  
CC form displays cell death repressor activity, whereas the short  
CC isoform promotes apoptosis (By similarity).  
CC -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear  
CC envelope (By similarity).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Long;  
CC IsoId=Q07816-1; Sequence=Displayed;  
CC : Name=Short;  
CC IsoId=Q07816-2; Sequence=VSP\_000514;  
CC -1- TISSUE SPECIFICITY: Highest expression in organs with lymphoid  
CC development.  
CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic  
CC function. Intact BH1 and BH2 domains are required for anti-  
CC apoptotic activity (By similarity).  
CC -1- SIMILARITY: Belongs to the Bcl-2 family.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; Z23110; CAA80657.1; -.  
DR EMBL; U26645; AAB07677.1; -.  
DR PIR; A47537; A47537.  
DR HSSP; P53563; IAF3.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
KW Alternative splicing; Apoptosis; Transmembrane.



FT	DOMAIN	4	24	BH4.
FT	DOMAIN	82	96	BH3.
FT	DOMAIN	125	144	BH1.
FT	DOMAIN	176	191	BH2.
FT	TRANSMEM	206	223	Potential.
FT	VARSPLIC	185	229	ERFVDLYGNNAAEELRKQETFNKMLLTGATVAGVLLLGSL LSRK -> VRTALP (in isoform short).
FT				/FTid=VSP_000514.
SQ	SEQUENCE	229 AA;	25733 MW;	A97D3A4D04C0E9DA CRC64;
	Query Match		42.9%;	Score 432.5; DB 1; Length 229;
	Best Local Similarity		41.7%;	Pred. No. 1.4e-30;
	Matches	95;	Conservative	22; Mismatches 62; Indels 49; Gaps 4;
OY	11 RALVADFVGyKLrOKGY-----VCgAgPGEGP-----			37
Db	6 RELVIDFVSyKLSQRGHcWSELEEDENRDTAAEAEmDSVLNGSPSWHPRPAGHVNGAT			65
OY	38 -----AADPLHQAmBAGDEFETRFRRTFSDLAQlHTVPGSaQQORFTQVSDE			85
Db	66 VHRSSLEVHEIVRASDVrQAALRDAGDEFELRYRRAFSDLTSGlHTTPGTAYQSFEQvVNE			125
OY	86 LFQGSPNwGRlVAFFVEFGAlCAESVNkEMEPLVGQvQEWNVAYLETRLADWIHSSGGWA			145
Db	126 LPHDGVNWGRIVAFfSFGAlCVESVDKEmRVLVGRIVSwMTTYLLTDHLDPwiQENGWE			185
OY	146 EFTALYGdGalEEARRLREGnNASVrTVLTGAVALGAlVTVGAFfFASk			193
Db	186 RFVDLYGNNA---AAELRKQETFNKMLLTGATVAGVLL-LGSLLSRK			229

RESULT 14	BCLX_PIG	STANDARD;	PRT;	233 AA.
ID	BCLX_PIG			
DT	077737;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).			
GN	Name=BCL2L1; Synonyms=BCLX, BLC2L;			
OS	Sus scrofa (pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99171363; PubMed=10072723; DOI=10.1006/jmcc.1998.0855;			
RA	Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Damer D.;			
RT	"Quantification of cardioprotective gene expression in porcine short-term hibernating myocardium.";			
RL	J. Mol. Cell. Cardiol. 31:147-158(1999).			
CC	-1- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-apoptotic activity is inhibited by association with SIVA isoform 1. Inhibits activation of caspases (By similarity). Appears to regulate cell death by blocking the voltage-dependent anion channel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane.			
CC	-1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By similarity). Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (By similarity). Isoform Bcl-X(L) binds to SIVA isoform 1 (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear envelope (By similarity).			
CC	-1- DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization with other Bcl-2 family members and for repression of cell death.			
CC	-1- PTM: Proteolytically cleaved by caspases during apoptosis (By similarity). The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity (By similarity).			
CC	-1- SIMILARITY: Belongs to the Bcl-2 family.			
CC	-1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.			
CC	-1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.			
CC	-1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.			

```

CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ001203; CAA04597.1; -.
DR HSSP; Q07817; 1MAZ.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR TIGRfams; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
DR Apoptosis; Mitochondrion; Transmembrane.
KW Apoptosis; Mitochondrion; Transmembrane.
FT DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.
FT DOMAIN 180 195 BH2.
FT TRANSMEM 210 226 Potential.
SQ SEQUENCE 233 AA; 26061 MW; 18BF6FA0441912B2 CRC64;

```

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Query Match          42.9%; Score 431.5; DB 1; Length 233;
Best Local Similarity 41.8%; Pred. NO. 1.7e-30;
Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;

QY      11 RALVADFVGYKLRQKGY-----V 28
      ||| |||: ||| |||
Db       6 RELVDFLSYKLSQKGYSWSQFTDVEENRTEAPGTESEAETPSAINGNSWHLADSPAV 65
      ||| |||: ||| |||

QY      29 CGAGPGEPPAD-----PLHQAMRAAGDEFFETRFRRTFSDLAQLHTVPGSAOQRT 80
      ||| |||: ||| |||
Db       66 NGA-TGHSSSLDAREVIMPAAVKQALREAGDEFELRYYRAFSDLTSQLHTPGTAYQSF 124
      ||| |||: ||| |||

QY      81 QVSDELFOGPPNNGRLVAFVFFGAALCAESVKNKMEPLVGQVQEWMAVLETRLADWIHS 140
      ||| |||: ||| |||
Db      125 QVLNELFRDGVNMGRIVAFSFGALCVESVDKEMQVLVSRIATWMTATYLNHLEPWIOE 184
      ||| |||: ||| |||

QY      141 SGGWAEFTALYGDGALBEARLRE--GNWASVTVLTGAVALLGAL 183
      ||| |||: ||| |||
Db      185 NGGWDTFVELYGNNAAAESRKQGERFNRNFLTGMTLAGVLLGSL 229
      ||| |||: ||| |||

RESULT 15
Q9N1A2
Q9N1A2      PRELIMINARY; PRT; 233 AA.
AC  Q9N1A2;
DT  01-OCT-2000 (TREMBlrel. 15, Created)
DT  01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT  01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DN  Anti-apoptotic regulator Bcl-XL.
GN  Name=bcl-xL;
OS  Sus scrofa (Pig).
OC  Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sub.
OX  NCBI_TaxID=9823;
RX  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Heart;
RA  Lee T.L., Cauty J.M.;
RL  Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF216205; AAF33212.1; -.

```

DR HSSP; Q07817; 1R2D.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; Bcl2\_family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRfams; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
SQ SEQUENCE 233 AA; 26047 MW; 2FA312818B25E17D CRC64;

Query Match 42.9%; Score 431.5; DB 2; Length 233;  
Best Local Similarity 41.8%; Pred. No. 1.7e-30;  
Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;

OY 11 RALVADFVGYKLRQKGY-----V 28  
Db 6 RELVVDFLSYKLSQKGYSGWQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV 65  
OY 29 CGAGPGEPPAD-----PLHQAMRAAGDEFETRFRRTFSDLAQLHVTGSAQQRFT 80  
Db 66 NGA-TGHSSSLDAREVTPMAAVKQALREAGDEFELRYRRAFSDLTSLHITPGTAYQSFE 124  
OY 81 QVSDLLFQGGPNWGRVAFVFGAALCAESVNKEMEPLVGVQVQEMWVAYLETRLADWIHS 140  
Db 125 QVNVNELFRDGVNWGRIVAFSFGALCVESVDKEMQVLVSRIATWMTATYLNHLEPWIOE 184  
OY 141 SGGWAEFTALYGDALAEARLRLE--GNWASVRTVLTGAVALGAL 183  
Db 185 NGGWDTFVELLYGNNAAESRKQGERFNRWFLTGMTLAGVLLGSL 229

Search completed: April 10, 2005, 22:42:53  
Job time : 61 secs

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OM protein - protein search, using sw model

Run on: April 10, 2005, 20:12:38 ; Search time 65 Seconds  
(without alignments)  
1148.381 Million cell updates/sec

Title: US-09-925-674B-7

Perfect score: 1007  
Sequence: 1 MATPASAPDTRALVADFGVY.....LTGAVALGALVTGAFPAASK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1:	Geneseqp19808:*
2:	Geneseqp19908:*
3:	Geneseqp20008:*
4:	Geneseqp20018:*
5:	Geneseqp20028:*
6:	Geneseqp20038:*
7:	Geneseqp2003bs:*
8:	Geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1007	100.0	193	2	AAY05530	Aay05530 Human Bcl
2	1007	100.0	193	7	ADD46742	Add46742 Human Pro
3	1007	100.0	193	8	ADP88349	Adp88349 Human Bcl
4	1002	99.5	193	2	AAW61392	Aaw61392 Human bcl
5	1002	99.5	193	2	AAW97392	Aaw97392 The human
6	1000	99.3	193	2	AAW36047	Aaw36047 Human bcl
7	1000	99.3	193	2	AAY05532	Aay05532 Human Bcl
8	1000	99.3	193	2	AAY05531	Aay05531 Mouse Bcl
9	997	99.0	192	2	AAW97394	Aaw97394 Mammalian
10	996	98.9	193	2	AAW61391	Aaw61391 Rat bcl-y
11	996	98.9	193	2	AAW97393	Aaw97393 The rat b
12	991	98.4	192	2	AAW97393	AAW97393 Protein s
13	958.5	95.2	192	2	AAY05533	Aay05533 Mouse Bcl
14	954	94.7	183	8	ADP88350	Adp88350 Derivativ
15	867	86.1	168	2	AAW36048	Aaw36048 Mouse bcl
16	821.5	81.6	190	5	AAO18223	Aao18223 Human bcl
17	766	76.1	365	2	AAW59884	Aaw59884 Amino aci
18	766	76.1	365	5	ABG95556	Abg95556 Human nov
19	766	76.1	365	6	ABO34750	Abg95556 Human nov
20	766	76.1	365	7	AD123411	Adi23411 Novel hum
21	766	76.1	365	8	ADH74413	Adh74413 Human sec
22	764.5	75.9	185	8	ABM84148	Abm84148 Human dia
23	457.5	45.4	179	8	ADH52635	Adh52635 Chinese h
24	448.5	44.5	199	8	ADH52637	Adh52637 Chinese h
25	441.5	43.8	219	8	ADH52639	Adh52639 Chinese h

26	436.5	43.3	219	8	ADH52641	Adh52641 Chinese h
27	435.5	43.2	342	8	ADQ97763	Adq97763 Mouse can
28	433.5	43.0	411	4	AAU00219	Aau00219 Bcl-XL-DT
29	431.5	42.9	233	8	ADQ80679	Adq80679 Porcine a
30	431.5	42.9	237	5	ABG78480	Abg78480 Wild type
31	429.5	42.7	233	8	ADH52633	Adh52633 Chinese h
32	428.5	42.6	233	2	AAR68887	Aar68887 Human thy
33	428.5	42.6	233	2	AAW05821	Aaw05821 Bcl-XL pr
34	428.5	42.6	233	2	AAW31530	Aaw31530 Human ant
35	428.5	42.6	233	3	AAy69969	Aay69969 Human Bcl
36	428.5	42.6	233	3	AAy83223	Aay83223 Bcl-x pol
37	428.5	42.6	233	4	AAb50538	Aab50538 Human Bcl
38	428.5	42.6	233	4	AAb73303	Aab73303 Rat wild-
39	428.5	42.6	233	4	AAg64262	Aag64262 Human Bcl
40	428.5	42.6	233	4	AAb47515	Aab47515 Protein e
41	428.5	42.6	233	7	ADE62921	Ade62921 Rat Prote
42	428.5	42.6	233	7	ADE62493	Ade62493 Human Pro
43	428.5	42.6	233	7	ADE62491	Ade62491 Rat Prote
44	428.5	42.6	233	7	ABW02410	Abw02410 Human Bcl
45	428.5	42.6	233	8	ADM45995	Adm45995 Human apo

ALIGNMENTS

RESULT 1	
AAAY05530	standard; protein; 193 AA.
ID	AAAY05530
XX	
AC	AAAY05530;
XX	
DT	05-JUL-1999 (first entry)
XX	
DE	Human Bcl-w protein essential for spermatogenesis.
XX	
KW	Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
KW	animal model.
XX	
OS	Homo sapiens.
XX	
PN	WO9913710-A1.
XX	
PD	25-MAR-1999.
XX	
PF	16-SEP-1998; 98WO-AU000764.
XX	
PR	16-SEP-1997; 97AU-00009228.
XX	
PA	(HAL-) HAL INST MEDICAL RES WALTER & ELIZA.
XX	
PI	Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX	
DR	WPI; 1999-243890/20.
DR	N-PSDB; AAX25132.
XX	
PT	An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT	protein associated with Bcl-w.
XX	
PS	Claim 2; Page 33; 52pp; English.
XX	
CC	The present sequence is human Bcl-w, a pro-survival member of the Bcl-2
CC	family which is widely expressed and which is essential for
CC	spermatogenesis. The invention relates generally to a method of treatment
CC	and to an animal model for the identification of molecules and genetic
CC	sequences useful for inducing or reducing fertility of male animals.
CC	Methods are provided for the treatment of infertility, or for reducing
CC	fertility, by modulating spermatogenesis. An animal model carries a
CC	mutation is at least one allele of the human or murine bcl-w gene (see
CC	AAX25132-35) or in a gene associated with bcl-w. Such animals have
CC	disorganised seminiferous tubules and are substantially infertile, but
CC	possess no other major abnormalities as determined by histological
CC	examination. They can be used to screen for therapeutic molecules
CC	including genetic sequences capable of inducing, enhancing or otherwise

CC facilitating spermatogenesis in animals, or which can induce infertility  
XX Sequence 193 AA;  
SQ

Query Match 100.0%; Score 1007; DB 2; Length 193;  
Best Local Similarity 100.0%; Pred. No. 1.8e-102;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAQQLHVTGPSAQORFTQVSDELFOGGPWNWRLVAFVFGAALCAESVNKEMEPLVG 120  
DB 61 FSDLAQQLHVTGPSAQORFTQVSDELFOGGPWNWRLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVOEWMVAYLETRLADWIHSSGWAFFETALYGDGALBEARRLREGNWSVRTVLTGAVAL 180  
DB 121 QVOEWMVAYLETRLADWIHSSGWAFFETALYGDGALBEARRLREGNWSVRTVLTGAVAL 180  
QY 181 GALVTGAFPAASK 193  
DB 181 GALVTGAFPAASK 193

RESULT 2  
ADD46742  
ID ADD46742 standard; protein; 193 AA.  
XX  
AC ADD46742;  
XX  
DT 02-DEC-2004 (revised)  
DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein Q92843, SEQ ID NO 12427.  
XX  
KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
OS Homo sapiens.  
OS Unidentified.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
DR WPI; 2003-268312/26.  
DR GENBANK; Q92843.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
PS Example 1; Page; 1017pp; English.  
XX  
CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (described in Table 3  
CC of the specification) which is differentially expressed during pain.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 193 AA;

Query Match 100.0%; Score 1007; DB 7; Length 193;  
Best Local Similarity 100.0%; Pred. No. 1.8e-102;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAQQLHVTGPSAQORFTQVSDELFOGGPWNWRLVAFVFGAALCAESVNKEMEPLVG 120  
DB 61 FSDLAQQLHVTGPSAQORFTQVSDELFOGGPWNWRLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVOEWMVAYLETRLADWIHSSGWAFFETALYGDGALBEARRLREGNWSVRTVLTGAVAL 180  
DB 121 QVOEWMVAYLETRLADWIHSSGWAFFETALYGDGALBEARRLREGNWSVRTVLTGAVAL 180  
QY 181 GALVTGAFPAASK 193  
DB 181 GALVTGAFPAASK 193

RESULT 3  
ADP88349  
ID ADP88349 standard; protein; 193 AA.  
XX  
AC ADP88349;  
XX  
DT 09-SEP-2004 (first entry)  
DT 09-SEP-2004 (first entry)  
XX  
DE Human Bcl-w protein.  
XX  
KW Bcl-w; human; protein structure; protein co-ordinate data.  
KW Homo sapiens.  
XX  
OS Homo sapiens.  
XX  
PN WO2004050697-A1.  
XX  
PD 17-JUN-2004.  
XX  
PF 03-DEC-2003; 2003WO-AU001624.  
XX  
PR 03-DEC-2002; 2002AU-00953259.  
XX  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX  
PI Hinds MG, Huang DCS, Day CL;  
XX  
DR WPI; 2004-487529/46.  
XX  
PT Solution useful for identifying or selecting agents that are capable of



PT Inhibiting biological activity of Bcl-w, comprises molecule that has Bcl-w active site defined by specific structure coordinates of Bcl-w amino acid residues.

XX Disclosure; Page 804-805; 810pp; English.

CC The present invention relates to a solution comprising a molecule or CC molecular complex that comprises at least a fragment of Bcl-w. Also CC disclosed is the structure of Bcl-w, in the form of protein coordinate CC data. The solution is useful for identifying, selecting or designing CC agents that are capable of inhibiting or potentiating one or more CC biological activity of Bcl-w, and in solving the structures of other CC proteins with similar structure. It is also useful for characterizing the CC three-dimensional structure of the Bcl-w molecule, molecular complex or CC its derivative. The present sequence is the human Bcl-w protein.

XX SQ Sequence 193 AA;

Query Match 100.0%; Score 1007; DB 8; Length 193;  
Best Local Similarity 100.0%; Pred. No. 1.8e-102;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60

DB 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60

OY 61 FSDLAQAQLHTVTPGSAQORFTQVSDELFOGQPNWGRLLVAFVFGAALCAESVNKEMEPLVG 120

DB 61 FSDLAQAQLHTVTPGSAQORFTQVSDELFOGQPNWGRLLVAFVFGAALCAESVNKEMEPLVG 120

OY 121 QVOEWMVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTLGTGAVAL 180

DB 121 QVOEWMVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTLGTGAVAL 180

OY 181 GALVTVGAFPAK 193

DB 181 GALVTVGAFPAK 193

RESULT 4

AAW61392

ID AAW61392 standard; protein; 193 AA.

XX AC AAW61392;

DT 02-OCT-1998 (first entry)

DE Human bcl-y protein.

KW bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.

OS Homo sapiens.

PN US5789201-A.

PD 04-AUG-1998.

PF 11-FEB-1997; 97US-00798897.

PR 23-FEB-1996; 96US-0012201P.

PA (COCE-) COCENSYS INC.

PI Guastella J;

DR WPI; 1998-446079/38.

DR N-PSDB; AAV28334.

PT Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell growth e.g. cancers.

PS Example; Column 17/18; 27pp; English.

XX CC The mammalian bcl-y protein is a member of the bcl-2 family, components CC in the cell death pathway. The bcl-2 family have both apoptotic activity CC and the apoptosis blocking activity. bcl-y falls in the apoptosis CC activity category. The recombinant protein may be used to prevent CC uncontrolled cell growth, either by its direct administration to CC recombinant genetic constructs to increase its expression in vivo. Also, CC antisense constructs can be used in disorders where prevention of cell CC death is desired

XX SQ Sequence 193 AA;

Query Match 99.5%; Score 1002; DB 2; Length 193;  
Best Local Similarity 99.5%; Pred. No. 6.6e-102;  
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60

DB 1 MATPASAPDTRALVEDFGVGYKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60

OY 61 FSDLAQAQLHTVTPGSAQORFTQVSDELFOGQPNWGRLLVAFVFGAALCAESVNKEMEPLVG 120

DB 61 FSDLAQAQLHTVTPGSAQORFTQVSDELFOGQPNWGRLLVAFVFGAALCAESVNKEMEPLVG 120

OY 121 QVOEWMVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTLGTGAVAL 180

DB 121 QVOEWMVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTLGTGAVAL 180

OY 181 GALVTVGAFPAK 193

DB 181 GALVTVGAFPAK 193

RESULT 5

AAW97392

ID AAW97392 standard; protein; 193 AA.

XX AC AAW97392;

DT 20-MAY-1999 (first entry)

DE The human bcl-y protein.

KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease; KW multiple sclerosis; myocardial infarction; vitally induced cell death; KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; KW premature cell death; cell death stimulator; prolonged cell life span; KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.

OS Homo sapiens.

PN US5883229-A.

PD 16-MAR-1999.

PF 25-NOV-1997; 97US-00978523.

PR 23-FEB-1996; 96US-0012201P.

PR 11-FEB-1997; 97US-00798897.

PA (COCE-) COCENSYS INC.

PI Guastella J;

DR WPI; 1999-214150/18.

DR N-PSDB; AAX15946.

PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for modulating programmed cell death.

PS Claim 1; Col 17-18; 26pp; English.

XX The present sequence represents human bcl-y protein (Hbcl-y). The  
CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-  
CC y are homologues of the bcl-2 protein thought to be involved in  
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y  
CC proteins may be used to treat conditions associated with a disruption of  
CC the cell death pathway. If they act as cell death inhibitors, they may be  
CC used in therapies to treat subjects suffering from: strokes, head trauma,  
CC Alzheimer's Disease, neural and muscular degenerative diseases  
CC (especially multiple sclerosis), myocardial infarction, vitally induced  
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis  
CC - conditions where cells under go premature cell death as a result of  
CC triggers which may or may not be apparent. They may also be used in this  
CC way to develop cell lines which remain viable in culture for an extended  
CC period. In contrast, if they act as cell death stimulators, Rbcl-y and  
CC Hbcl-y may be used to treat conditions associated with prolonged cell  
CC life span such as cancer (especially kaposi's sarcoma and lung cancer)  
CC and auto/hyperimmune diseases. They may also be used to cause cell death  
CC in, and hence control, parasites  
SQ Sequence 193 AA;

Query Match 99.5%; Score 1002; DB 2; Length 193;  
Best Local Similarity 99.5%; Pred. No. 6.6e-102;  
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 MATPASAPDTRALVADFGVGYKLROKGYVCAGPGEGPADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASAPDTRALVEDFVGKYLROKGYVCAGPGEGPADPLHQAMRAAGDEFETRFRRT 60  
OY 61 FSDLAQOLHVTTPGSAQQRFTQVSDELFOGPGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
DB 61 FSDLAQOLHVTTPGSAQQRFTQVSDELFOGPGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
OY 121 QVQEMWVAYLETRLADWIHSSGWAFFLTALYGDGALBEARRLREGNWSVRTLGTGAVAL 180  
DB 121 QVQEMWVAYLETRLADWIHSSGWAFFLTALYGDGALBEARRLREGNWSVRTLGTGAVAL 180  
OY 181 GALVTVGAFPAASK 193  
DB 181 GALVTVGAFPAASK 193

RESULT 6  
AAW36047  
ID AAW36047 standard; protein; 193 AA.  
AC AAW36047;  
XX  
DT 22-APR-1998 (first entry)  
XX  
DE Human bcl-w protein.  
XX  
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
KW diagnosis; degenerative disease.  
XX  
OS Homo sapiens.  
XX  
PN WO9735971-A1.  
XX  
PD 02-OCT-1997.  
XX  
PF 27-MAR-1997; 97WO-AU0001199.  
XX  
PR 27-MAR-1996; 96AU-00008965.  
XX  
PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX  
PI Cory S, Adams JM, Gibson LM, Holmgreen SP;  
XX  
DR WPI; 1997-489635/45.  
DR N-PSDB; AAT96577.  
XX

PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or  
PT inhibit cell survival, e.g. for treatment of cancer and degenerative  
PT diseases.  
XX  
PS Claim 6; Page 48; 86pp; English.  
XX  
XX This sequence represents a novel human protein, bcl-w, encoded by the bcl  
CC -2 gene family and extracted from an adult brain library. This gene  
CC promotes cell survival, so its modulation is useful in treatment of  
CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,  
CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,  
CC ischaemia, human immunodeficiency virus infection or in cell transplants.  
CC Up-regulation of the gene can also be used to modify cell lines cultured  
CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas  
CC and to increase survival of primary explants during genetic modification.  
CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,  
CC antibody production or screening of potential modulators  
SQ Sequence 193 AA;

Query Match 99.3%; Score 1000; DB 2; Length 193;  
Best Local Similarity 99.0%; Pred. No. 1.1e-101;  
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
OY 1 MATPASAPDTRALVADFGVGYKLROKGYVCAGPGEGPADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASAPDTRALVADFGVGYKLROKGYVCAGPGEGPADPLHQAMRAAGDEFETRFRRT 60  
OY 61 FSDLAQOLHVTTPGSAQQRFTQVSDELFOGPGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
DB 61 FSDLAQOLHVTTPGSAQQRFTQVSDELFOGPGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
OY 121 QVQEMWVAYLETRLADWIHSSGWAFFLTALYGDGALBEARRLREGNWSVRTLGTGAVAL 180  
DB 121 QVQEMWVAYLETRLADWIHSSGWAFFLTALYGDGALBEARRLREGNWSVRTLGTGAVAL 180  
OY 181 GALVTVGAFPAASK 193  
DB 181 GALVTVGAFPAASK 193

RESULT 7  
AAY05532  
ID AAY05532 standard; protein; 193 AA.  
AC AAY05532;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Human Bcl-w protein essential for spermatogenesis.  
XX  
KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;  
KW animal model.  
XX  
OS Homo sapiens.  
XX  
PN WO9913710-A1.  
XX  
PD 25-MAR-1999.  
XX  
PF 16-SEP-1998; 98WO-AU000764.  
XX  
PR 16-SEP-1997; 97AU-00009228.  
XX  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX  
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;  
XX  
DR WPI; 1999-243890/20.  
DR N-PSDB; AAX25134.  
XX  
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
PT protein associated with Bcl-w.

XX Disclosure; Page 37; 52pp; English.  
 PS  
 CC The present sequence is described of a derivative of human Bcl-w (see  
 CC also AAY05530), a pro-survival member of the Bcl-2 family that is widely  
 CC expressed and which is essential for spermatogenesis. The invention  
 CC relates generally to a method of treatment and to an animal model for the  
 CC identification of molecules and genetic sequences useful for inducing or  
 CC reducing fertility of male animals. Methods are provided for the  
 CC treatment of infertility, or for reducing fertility, by modulating  
 CC spermatogenesis. An animal model carries a mutation is at least one  
 CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene  
 CC associated with bcl-w. Such animals have disorganised seminiferous tubules  
 CC and are substantially infertile, but possess no other major abnormalities  
 CC as determined by histological examination. They can be used to screen for  
 CC therapeutic molecules including genetic sequences capable of inducing,  
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which  
 CC can induce infertility

XX  
 SQ Sequence 193 AA;

Query Match 99.3%; Score 1000; DB 2; Length 193;  
 Best Local Similarity 99.0%; Pred. No. 1.1e-101;  
 Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60  
 |||  
 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60  
 DB 61 FSDLAOLHTVTPGSAQORFTQVSDELFOGSPNMGRLVAFVFGAALCAESVNKEMEPLVG 120  
 |||  
 61 FSDLAOLHTVTPGSAQORFTQVSDELFOGSPNMGRLVAFVFGAALCAESVNKEMEPLVG 120  
 OY 121 QVQEWNVAYLETRLADWIHSSSGMAEFTALYGDGALBEARRLREGNMAVVRTVLTGAVAL 180  
 |||  
 121 QVQEWNVAYLETRLADWIHSSSGMAEFTALYGDGALBEARRLREGNMAVVRTVLTGAVAL 180  
 DB 121 QVQEWNVAYLETRLADWIHSSSGMAEFTALYGDGALBEARRLREGNMAVVRTVLTGAVAL 180  
 |||  
 121 QVQEWNVAYLETRLADWIHSSSGMAEFTALYGDGALBEARRLREGNMAVVRTVLTGAVAL 180  
 OY 181 GALVTVGAFPAASK 193  
 |||  
 181 GALVTVGAFPAASK 193  
 DB 181 GALVTVGAFPAASK 193

RESULT 8  
 AAY05531  
 ID AAY05531 standard; protein; 193 AA.  
 XX  
 AC AAY05531;  
 XX  
 DT 05-JUL-1999 (first entry)  
 XX  
 DE Mouse Bcl-w protein essential for spermatogenesis.  
 XX  
 KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;  
 KW animal model.  
 XX  
 OS Mus sp.  
 XX  
 PN WO913710-A1.  
 XX  
 PD 25-MAR-1999.  
 XX  
 PF 16-SEP-1998; 98WO-AU000764.  
 XX  
 PR 16-SEP-1997; 97AU-00009228.  
 XX  
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
 XX  
 PI Cory S, Adams J, Print C, Gibson L, Koentgen F;  
 XX  
 DR WPI; 1999-243890/20.  
 DR N-PSDB; AAX25133.  
 XX  
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or

PT protein associated with Bcl-w.  
 XX  
 PS Claim 2; Page 35; 52pp; English.  
 XX

XX The present sequence is mouse Bcl-w, a pro-survival member of the Bcl-2  
 CC family which is widely expressed and which is essential for  
 CC spermatogenesis. The invention relates generally to a method of treatment  
 CC and to an animal model for the identification of molecules and genetic  
 CC sequences useful for inducing or reducing fertility of male animals.  
 CC Methods are provided for the treatment of infertility, or for reducing  
 CC fertility, by modulating spermatogenesis. An animal model carries a  
 CC mutation is at least one allele of the human or murine bcl-w gene (see  
 CC AAX25132-35) or in a gene associated with bcl-w. Such animals have  
 CC disorganised seminiferous tubules and are substantially infertile, but  
 CC possess no other major abnormalities as determined by histological  
 CC examination. They can be used to screen for therapeutic molecules  
 CC including genetic sequences capable of inducing, enhancing or otherwise  
 CC facilitating spermatogenesis in animals, or which can induce infertility

XX  
 SQ Sequence 193 AA;

Query Match 99.3%; Score 1000; DB 2; Length 193;  
 Best Local Similarity 99.0%; Pred. No. 1.1e-101;  
 Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60  
 |||  
 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60  
 DB 61 FSDLAOLHTVTPGSAQORFTQVSDELFOGSPNMGRLVAFVFGAALCAESVNKEMEPLVG 120  
 |||  
 61 FSDLAOLHTVTPGSAQORFTQVSDELFOGSPNMGRLVAFVFGAALCAESVNKEMEPLVG 120  
 OY 121 QVQEWNVAYLETRLADWIHSSSGMAEFTALYGDGALBEARRLREGNMAVVRTVLTGAVAL 180  
 |||  
 121 QVQEWNVAYLETRLADWIHSSSGMAEFTALYGDGALBEARRLREGNMAVVRTVLTGAVAL 180  
 DB 121 QVQEWNVAYLETRLADWIHSSSGMAEFTALYGDGALBEARRLREGNMAVVRTVLTGAVAL 180  
 |||  
 121 QVQEWNVAYLETRLADWIHSSSGMAEFTALYGDGALBEARRLREGNMAVVRTVLTGAVAL 180  
 OY 181 GALVTVGAFPAASK 193  
 |||  
 181 GALVTVGAFPAASK 193  
 DB 181 GALVTVGAFPAASK 193

RESULT 9  
 AAW97394  
 ID AAW97394 standard; protein; 192 AA.  
 XX  
 AC AAW97394;  
 XX  
 DT 20-MAY-1999 (first entry)  
 XX  
 DE Mammalian bcl-y protein.  
 XX  
 KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
 KW premature cell death; cell death stimulator; prolonged cell life span;  
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.  
 XX  
 OS Mammalia.  
 XX  
 PN US5883229-A.  
 XX  
 PD 16-MAR-1999.  
 XX  
 PF 25-NOV-1997; 97US-00978523.  
 XX  
 PR 23-FEB-1996; 96US-0012201P.  
 PR 11-FEB-1997; 97US-00798897.  
 XX  
 PA (COCE-) COCENSY INC.  
 XX

PI Guastella J;  
XX  
DR WPI; 1999-214150/18.  
XX  
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for  
PT modulating programmed cell death.  
XX  
PS Claim 2; Col 19-22; 26pp; English.  
XX  
CC The present sequence represents a mammalian bcl-1 protein. The  
CC specification describes rat bcl-y protein (Rbcl-y) and human bcl-y  
CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein  
CC thought to be involved in programmed cell death (apoptosis and necrosis).  
CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated  
CC with a disruption of the cell death pathway. If they act as cell death  
CC inhibitors, they may be used in therapies to treat subjects suffering  
CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular  
CC degenerative diseases (especially multiple sclerosis), myocardial  
CC infarction, vitally induced cell death, aging, spinal cord injuries and  
CC amyotrophic lateral sclerosis- conditions where cells under go premature  
CC cell death as a result of triggers which may or may not be apparent. They  
CC may also be used in this way to develop cell lines which remain viable in  
CC culture for an extended period. In contrast, if they act as cell death  
CC stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated  
CC with prolonged cell life span such as cancer (especially Kaposi's sarcoma  
CC and lung cancer) and auto/hyperimmune diseases. They may also be used to  
CC cause cell death in, and hence control, parasites  
XX  
SQ Sequence 192 AA;

Query Match 99.0%; Score 997; DB 2; Length 192;  
Best Local Similarity 99.5%; Pred. No. 2.3e-101;  
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 ATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRTF 61  
Db 1 ATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRTF 61  
QY 62 SDLAOLHVTTPGSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQ 60  
Db 61 SDLAOLHVTTPGSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQ 121  
QY 122 VOEWNVAYLETRLADWIHSSGGAFTALYGDGALBEARRLREGNMAVSRVTLTGAVALG 120  
Db 121 VOEWNVAYLETRLADWIHSSGGAFTALYGDGALBEARRLREGNMAVSRVTLTGAVALG 181  
QY 182 ALVTVGAFPAK 193  
Db 181 ALVTVGAFPAK 192

RESULT 10  
AAW61391  
ID AAW61391 standard; protein; 193 AA.  
XX  
AC AAW61391;  
XX  
DT 02-OCT-1998 (first entry)  
XX  
DE Rat bcl-y protein.  
XX  
KW bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.  
OS Rattus sp.  
XX  
PN US5789201-A.  
XX  
PD 04-AUG-1998.  
XX  
PF 11-FEB-1997; 97US-00798897.  
XX  
PR 23-FEB-1996; 96US-0012201P.

PA (COCE-) COCENSYS INC.  
XX  
PI Guastella J;  
XX  
DR WPI; 1998-446079/38.  
DR N-PSDB; AAV28333.  
XX  
PT Nucleic acids encoding B-cell lymphoma-y protein - useful for producing  
PT recombinant protein for use in treating uncontrolled cell growth e.g.  
PT cancers.  
XX  
PS Example; Fig 3A; 27pp; English.  
XX  
CC The mammalian bcl-y protein is a member of the bcl-2 family, components  
CC in the cell death pathway. The bcl-2 family have both apoptotic activity  
CC and the apoptosis blocking activity. bcl-y falls in the apoptosis  
CC activity category. The recombinant protein may be used to prevent  
CC uncontrolled cell growth, either by its direct administration to  
CC recombinant genetic constructs to increase its expression in vivo. Also,  
CC antisense constructs can be used in disorders where prevention of cell  
CC death is desired  
XX  
SQ Sequence 193 AA;

Query Match 98.9%; Score 996; DB 2; Length 193;  
Best Local Similarity 98.4%; Pred. No. 3e-101;  
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
Db 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAOLHVTTPGSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
Db 61 FSDLAOLHVTTPGSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 VOEWNVAYLETRLADWIHSSGGAFTALYGDGALBEARRLREGNMAVSRVTLTGAVAL 180  
Db 121 VOEWNVAYLETRLADWIHSSGGAFTALYGDGALBEARRLREGNMAVSRVTLTGAVAL 180  
QY 181 GALVTVGAFPAK 193  
Db 181 GALVTVGAFPAK 193

RESULT 11  
AAW97391  
ID AAW97391 standard; protein; 193 AA.  
XX  
AC AAW97391;  
XX  
DT 20-MAY-1999 (first entry)  
XX  
DE The rat bcl-y protein.  
XX  
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
KW premature cell death; cell death stimulator; prolonged cell life span;  
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.  
OS Rattus sp.  
XX  
PN US5883229-A.  
XX  
PD 16-MAR-1999.  
XX  
PF 25-NOV-1997; 97US-00978523.  
XX  
PR 23-FEB-1996; 96US-0012201P.  
PR 11-FEB-1997; 97US-00798897.



XX (COCE-) COCENSYS INC.  
PA Guastella J;  
XX  
PI MPI, 1999-214150/18.  
XX  
DR N-PSDB; AAX15945.  
XX  
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for  
PT modulating programmed cell death.  
XX  
PS Disclosure; Col 15-18; 26pp; English.  
XX  
CC The present sequence represents rat bcl-y protein (Rbcl-y). The  
CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and  
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in  
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y  
CC proteins may be used to treat conditions associated with a disruption of  
CC the cell death pathway. If they act as cell death inhibitors, they may be  
CC used in therapies to treat subjects suffering from: strokes, head trauma,  
CC Alzheimer's Disease, neural and muscular degenerative diseases  
CC (especially multiple sclerosis), myocardial infarction, vitally induced  
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis  
CC - conditions where cells under go premature cell death as a result of  
CC triggers which may or may not be apparent. They may also be used in this  
CC way to develop cell lines which remain viable in culture for an extended  
CC period. In contrast, if they act as cell death stimulators, Rbcl-y and  
CC Hbcl-y may be used to treat conditions associated with prolonged cell  
CC life span such as cancer (especially kaposi's sarcoma and lung cancer)  
CC and auto/hyperimmune diseases. They may also be used to cause cell death  
CC in, and hence control, parasites  
XX  
SQ Sequence 193 AA;  
  
Query Match 98.9%; Score 996; DB 2; Length 193;  
Best Local Similarity 98.4%; Pred. No. 3e-101;  
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASTPDRALVADFGVGYKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60  
  
QY 61 FSDLAQLHVTTPGSAQOQRTQVSDELFOGPGNMGRLVAFVFGAALCAESVNKEMEPLVG 120  
DB 61 FSDLAQLHVTTPGSAQOQRTQVSDELFOGPGNMGRLVAFVFGAALCAESVNKEMEPLVG 120  
  
QY 121 QVOEWMVAVYLETRLADWIHSSGGWAEFTALYGDALBEARRLREGNWSVRTLGTGAVAL 180  
DB 121 QVOEWMVAVYLETRLADWIHSSGGWAEFTALYGDALBEARRLREGNWSVRTLGTGAVAL 180  
  
QY 181 GALVTVGAFPAASK 193  
DB 181 GALVTVGAFPAASK 193  
  
RESULT 12  
AAW97393  
ID AAW97393 standard; protein; 192 AA.  
XX  
AC AAW97393;  
XX  
DT 20-MAY-1999 (first entry)  
XX  
DE Protein sequence of the specification.  
XX  
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
KW premature cell death; cell death stimulator; prolonged cell life span;  
KW kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.  
XX

OS Unidentified.  
XX  
XX US5883229-A.  
XX  
XX 16-MAR-1999.  
XX  
XX 25-NOV-1997; 97US-00978523.  
XX  
XX 23-FEB-1996; 96US-0012201P.  
XX 11-FEB-1997; 97US-00798897.  
XX  
XX (COCE-) COCENSYS INC.  
XX  
XX Guastella J;  
XX  
XX MPI, 1999-214150/18.  
XX  
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for  
PT modulating programmed cell death.  
XX  
PS Disclosure; Col 19-20; 26pp; English.  
XX  
CC The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y  
CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein  
CC thought to be involved in programmed cell death (apoptosis and necrosis).  
CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated  
CC with a disruption of the cell death pathway. If they act as cell death  
CC inhibitors, they may be used in therapies to treat subjects suffering  
CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular  
CC degenerative diseases (especially multiple sclerosis), myocardial  
CC infarction, vitally induced cell death, aging, spinal cord injuries and  
CC amyotrophic lateral sclerosis - conditions where cells under go premature  
CC cell death as a result of triggers which may or may not be apparent. They  
CC may also be used in this way to develop cell lines which remain viable in  
CC culture for an extended period. In contrast, if they act as cell death  
CC stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated  
CC with prolonged cell life span such as cancer (especially kaposi's sarcoma  
CC and lung cancer) and auto/hyperimmune diseases. They may also be used to  
CC cause cell death in, and hence control, parasites  
XX  
SQ Sequence 192 AA;  
  
Query Match 98.4%; Score 991; DB 2; Length 192;  
Best Local Similarity 98.4%; Pred. No. 1.1e-100;  
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 ATPASAPDTRALVADFGVGYKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 61  
DB 1 ATPASTPDRALVADFGVGYKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60  
  
QY 62 SDLAQLHVTTPGSAQOQRTQVSDELFOGPGNMGRLVAFVFGAALCAESVNKEMEPLVGQ 121  
DB 61 SDLAQLHVTTPGSAQOQRTQVSDELFOGPGNMGRLVAFVFGAALCAESVNKEMEPLVGQ 120  
  
QY 122 QVOEWMVAVYLETRLADWIHSSGGWAEFTALYGDALBEARRLREGNWSVRTLGTGAVALG 181  
DB 122 QVOEWMVAVYLETRLADWIHSSGGWAEFTALYGDALBEARRLREGNWSVRTLGTGAVALG 180  
  
QY 182 ALVTVGAFPAASK 193  
DB 181 ALVTVGAFPAASK 192  
  
RESULT 13  
AAV05533  
ID AAV05533 standard; protein; 192 AA.  
XX  
AC AAV05533;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Mouse Bcl-w protein derivative.  
XX



DT 22-APR-1998 (first entry)

DE Mouse bcl-w protein.

KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
 KW diagnosis; degenerative disease.

**OS Mus sp.**

OS Mus sp.

PN W09735971-A1.

PD 02-OCT-1997.

PF 27-MAR-1997; 97WO-AU000199.

PR 27-MAR-1996; 96AU-00008965.

PA (AMRA-) AMRAD OPERATIONS PTY LTD.

PI Cory S, Adams JM, Gibson LM, Holmgreen SP;

DR WPI: 1997-489635/45.

DR N-PSDB; AAT96578.

PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or  
PT inhibit cell survival, e.g. for treatment of cancer and degenerative  
PT diseases.

PS Claim 6; Page 50-51; 86pp; English.

**CC** This sequence represents a novel protein, bcl-w, encoded by the mouse bcl

CC useful in treatment of cancer or auto-immune diseases, degenerative

CC modify cell lines cultured in vivo, e.g. to develop new lines, to  
CC facilitate isolation of hybridomas and to increase survival of primary  
CC explants during genetic modification. It can be used to produce  
CC recombinant Bcl-w for therapy, diagnosis, antibody production or  
CC screening of potential modulators

**SQ Sequence 168: AA;**

Query Match	86.14	Score 867	DB 2	Length 168
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Matches 161; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPADPLHQAMRAAGDEFFETRFRRT 60

Db 1 MPTPASTPDRALVADFVGYRLRQKGYVCGAGPGECPADPLHQAMRAAGDEFETRFRRT 60

61 FSDLAQHLVTPGSAQRFTQVSDDELFGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120

Db 61 FSDLAQLHVTPCSAQRFTQVSDELFGGPNWGRVAFVFGAALCAESVNKEMEPLVG 120

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Db 121 QVQDWI VAYLETRLADWIHSSGGWADFTALYGDCAL EDARRLREGNWA 168

Job time : 68 secs

Db 121 QVQDWI VAYLETRLADWIHSSGGWADFTALYGDCAL EDARRLREGNWA 168

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 10, 2005, 22:43:04 ; Search time 227.5 Seconds  
(without alignments)  
281.650 Million cell updates/sec

Title: US-09-925-674B-7

Perfect score: 1007

Sequence: 1 MATPASAPDTRALVADFGVY.....LTGAVALGALVTGAFASK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA: \*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep: \*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep: \*  
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9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep: \*  
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16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep: \*  
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19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1007	100.0	193	9 US-09-925-674A-7	Sequence 7, Appli
2	1007	100.0	193	16 US-10-450-366-6	Sequence 6, Appli
3	997	99.0	193	9 US-09-925-674A-9	Sequence 9, Appli
4	766	76.1	365	10 US-09-809-391-696	Sequence 696, App
5	766	76.1	365	10 US-09-882-171-696	Sequence 696, App
6	766	76.1	365	15 US-10-164-861-696	Sequence 696, App
7	627.5	62.3	228	16 US-10-659-705-2	Sequence 2, Appli
8	457.5	45.4	179	15 US-10-402-017-6	Sequence 6, Appli
9	448.5	44.5	199	15 US-10-402-017-8	Sequence 8, Appli
10	441.5	43.8	219	15 US-10-402-017-10	Sequence 10, Appli
11	436.5	43.3	219	15 US-10-402-017-12	Sequence 12, Appli
12	433.5	43.0	411	16 US-10-792-517-2	Sequence 2, Appli
13	432.5	42.9	229	16 US-10-659-705-7	Sequence 7, Appli

14	429.5	42.7	233	15 US-10-402-017-4	Sequence 4, Appli
15	428.5	42.6	233	9 US-09-734-846-2	Sequence 2, Appli
16	428.5	42.6	233	9 US-09-952-278-6	Sequence 6, Appli
17	428.5	42.6	233	14 US-10-101-482-14	Sequence 14, Appli
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19	428.5	42.6	233	14 US-10-169-223-10	Sequence 10, Appli
20	428.5	42.6	233	14 US-10-302-262-2	Sequence 2, Appli
21	428.5	42.6	233	15 US-10-116-275-171	Sequence 171, App
22	428.5	42.6	233	16 US-10-450-366-5	Sequence 5, Appli
23	428.5	42.6	233	16 US-10-659-705-8	Sequence 8, Appli
24	416.5	41.4	239	15 US-10-148-953A-3	Sequence 3, Appli
25	415.5	41.3	152	14 US-10-158-769-2	Sequence 2, Appli
26	414.5	41.2	233	16 US-10-659-705-3	Sequence 3, Appli
27	413	41.0	236	13 US-10-087-192-1953	Sequence 1953, Ap
28	412.5	41.0	239	14 US-10-277-693A-10	Sequence 10, Appli
29	412.5	41.0	239	15 US-10-003-632C-10	Sequence 10, Appli
30	412.5	41.0	239	15 US-10-003-632C-13	Sequence 13, Appli
31	410.5	40.8	239	8 US-08-726-211-5	Sequence 5, Appli
32	410.5	40.8	239	10 US-09-993-420A-8	Sequence 8, Appli
33	410.5	40.8	239	14 US-10-101-482-12	Sequence 12, Appli
34	410.5	40.8	239	14 US-10-072-830-2	Sequence 2, Appli
35	410.5	40.8	239	14 US-10-141-618-12	Sequence 12, Appli
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37	410.5	40.8	239	15 US-10-387-961A-5	Sequence 5, Appli
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39	410.5	40.8	239	15 US-10-003-632C-3	Sequence 3, Appli
40	410.5	40.8	239	15 US-10-148-953A-1	Sequence 1, Appli
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42	410.5	40.8	239	15 US-10-297-321-2	Sequence 2, Appli
43	410.5	40.8	239	16 US-10-450-366-4	Sequence 4, Appli
44	410.5	40.8	239	16 US-10-770-668-16	Sequence 16, Appli
45	410.5	40.8	485	16 US-10-792-517-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1  
US-09-925-674A-7  
; Sequence 7, Application US/09925674A  
; Patent No. US20020119943A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
; FILE REFERENCE: 11686a  
; CURRENT APPLICATION NUMBER: US/09/925, 674A  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/925, 674  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: PN8965  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-09-925-674A-7

QY	1	MATPASAPDTRALVADFGVYKLRQKGYCGAGPBGPAADPLHQAMRAAGDEFETRFRRT	60
DB	1	MATPASAPDTRALVADFGVYKLRQKGYCGAGPBGPAADPLHQAMRAAGDEFETRFRRT	60
QY	61	FSDLAQQLHTVTPGSAQQRFTQVSDLEFGGPNWGRVAFVFGAALCAESVNKMEPLVG	120
DB	61	FSDLAQQLHTVTPGSAQQRFTQVSDLEFGGPNWGRVAFVFGAALCAESVNKMEPLVG	120
QY	121	QVQEWNVAVLETRLADWIHSSGWAETALYGDGALBEARRLREGNWSVRTVLTGAVAL	180

Db 121 QVQEMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTLGAVAL 180  
QY 181 GALVTGAFPAASK 193  
Db 181 GALVTGAFPAASK 193

RESULT 2

US-10-450-366-6  
; Sequence 6, Application US/10450366  
; Publication No. US20040115667A1  
; GENERAL INFORMATION:  
; APPLICANT: Tschopp, Jorg  
; APPLICANT: Hoffmann, Kay  
; TITLE OF INVENTION: DNA-Sequences, Which Code For An Apoptosis Signal Transduction Pr  
; FILE REFERENCE: 11436\*3  
; CURRENT APPLICATION NUMBER: US/10/450,366  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: PCT/EP01/14597  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: DE 100 61 766.2  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: DE 101 00 280.7  
; PRIOR FILING DATE: 2001-01-04  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human Bcl-W  
US-10-450-366-6

Query Match 100.0%; Score 1007; DB 16; Length 193;  
Best Local Similarity 100.0%; Pred. No. 7.9e-97;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
Db 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAALQLHTVTPGSAQQRFTQVSDELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
Db 61 FSDLAALQLHTVTPGSAQQRFTQVSDELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQEMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTLGAVAL 180  
Db 121 QVQEMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTLGAVAL 180  
QY 181 GALVTGAFPAASK 193  
Db 181 GALVTGAFPAASK 193

RESULT 3

US-09-925-674A-9  
; Sequence 9, Application US/09925674A  
; Patent No. US20020119943A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES  
; FILE REFERENCE: 11686a  
; CURRENT APPLICATION NUMBER: US/09/925,674A  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/925,674  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: PN8965  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-925-674A-9

Query Match 99.0%; Score 997; DB 9; Length 193;  
Best Local Similarity 98.4%; Pred. No. 8.7e-96;  
Matches 190; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
Db 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAALQLHTVTPGSAQQRFTQVSDELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
Db 61 FSDLAALQLHTVTPGSAQQRFTQVSDELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQEMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTLGAVAL 180  
Db 121 QVQEMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTLGAVAL 180  
QY 181 GALVTGAFPAASK 193  
Db 181 GALVTGAFPAASK 193

RESULT 4

US-09-809-391-696  
; Sequence 696, Application US/09809391  
; Publication No. US20030049618A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/809,391  
; CURRENT FILING DATE: 2001-03-16  
; Prior application data removed - consult PAM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 696  
; LENGTH: 365  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-809-391-696

Query Match 76.1%; Score 766; DB 10; Length 365;  
Best Local Similarity 100.0%; Pred. No. 2.7e-71;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
Db 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAALQLHTVTPGSAQQRFTQVSDELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
Db 61 FSDLAALQLHTVTPGSAQQRFTQVSDELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQEMWVAYLETRLADWIHSSGGW 144  
Db 121 QVQEMWVAYLETRLADWIHSSGGW 144

RESULT 5

US-09-882-171-696  
; Sequence 696, Application US/09882171  
; Publication No. US20030175858A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/882,171  
; CURRENT FILING DATE: 2001-06-18



;; PRIOR APPLICATION NUMBER: 60/047,586  
;; PRIOR FILING DATE: 1997-05-23  
;; PRIOR APPLICATION NUMBER: 60/047,590  
;; PRIOR FILING DATE: 1997-05-23  
;; PRIOR APPLICATION NUMBER: 60/047,594  
;; PRIOR FILING DATE: 1997-05-23  
;; PRIOR APPLICATION NUMBER: 60/047,589  
;; PRIOR FILING DATE: 1997-05-23  
;; PRIOR APPLICATION NUMBER: 60/047,593  
;; PRIOR FILING DATE: 1997-05-23  
;; PRIOR APPLICATION NUMBER: 60/047,614  
;; PRIOR FILING DATE: 1997-05-23  
;; PRIOR APPLICATION NUMBER: 60/043,578  
;; PRIOR FILING DATE: 1997-04-11  
;; PRIOR APPLICATION NUMBER: 60/043,576  
;; PRIOR FILING DATE: 1997-04-11  
;; PRIOR APPLICATION NUMBER: 60/047,501  
;; PRIOR FILING DATE: 1997-05-23  
;; PRIOR APPLICATION NUMBER: 60/043,670  
;; PRIOR FILING DATE: 1997-04-11  
;; PRIOR APPLICATION NUMBER: 60/056,632  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,664  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,876  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,881  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,909  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,875  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,862  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,887  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,908  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/048,964  
;; PRIOR FILING DATE: 1997-06-06  
;; PRIOR APPLICATION NUMBER: 60/057,650  
;; PRIOR FILING DATE: 1997-09-05  
;; PRIOR APPLICATION NUMBER: 60/056,884  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/057,669  
;; PRIOR FILING DATE: 1997-09-05

Query Match  
Best Local Similarity 76.1%; Score 766; DB 10; Length 365;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGVYKLRQKGYVCAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASAPDTRALVADFGVYKLRQKGYVCAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAQLHVTTPGSAQQRFTQVSDELFOGSPNMGRLVAFVFGAALCAESVNKEMEPLVG 120  
DB 61 FSDLAQLHVTTPGSAQQRFTQVSDELFOGSPNMGRLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQEMWVAYLETRLADWIHSSGGW 144  
DB 121 QVQEMWVAYLETRLADWIHSSGGW 144

RESULT 6  
US-10-164-861-696  
Sequence 696, Application US/10164861  
Publication No. US20030225248A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT APPLICATION NUMBER: US/10/164,861

;; CURRENT FILING DATE: 2002-06-10  
;; PRIOR APPLICATION NUMBER: US/09/149,476  
;; PRIOR FILING DATE: 1998-09-08  
;; PRIOR APPLICATION NUMBER: PCT/US98/04493  
;; PRIOR FILING DATE: 1998-03-06  
;; NUMBER OF SEQ ID NOS: 757  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 696  
;; LENGTH: 365  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-164-861-696

Query Match  
Best Local Similarity 76.1%; Score 766; DB 15; Length 365;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGVYKLRQKGYVCAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASAPDTRALVADFGVYKLRQKGYVCAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAQLHVTTPGSAQQRFTQVSDELFOGSPNMGRLVAFVFGAALCAESVNKEMEPLVG 120  
DB 61 FSDLAQLHVTTPGSAQQRFTQVSDELFOGSPNMGRLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQEMWVAYLETRLADWIHSSGGW 144  
DB 121 QVQEMWVAYLETRLADWIHSSGGW 144

RESULT 7  
US-10-659-705-2  
Sequence 2, Application US/10659705  
Publication No. US20040117867A1  
GENERAL INFORMATION:  
APPLICANT: Look, A. Thomas  
TITLE OF INVENTION: Transgenic Cancer Models in Fish  
FILE REFERENCE: 112706.123  
CURRENT APPLICATION NUMBER: US/10/659,705  
PRIOR FILING DATE: 2003-09-11  
PRIOR APPLICATION NUMBER: US 60/409,585  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 228  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: BCL2 proteins  
US-10-659-705-2

Query Match  
Best Local Similarity 62.3%; Score 627.5; DB 16; Length 228;  
Matches 123; Conservative 21; Mismatches 37; Indels 3; Gaps 1;

QY 10 TRALVADFGVYKLRQKGYVCAGPGEPAADPLHQAMRAAGDEFETRFRRTSDLAQLH 69  
DB 48 SRALVEDLVRYKLCGRSLV--PSPGAAALCAESVNKEMEPLVGQVQEMWVAY 129  
QY 70 VTPGSAQQRFTQVSDELFOGSPNMGRLVAFVFGAALCAESVNKEMEPLVGQVQEMWVAY 129  
DB 105 VTPGTAIARFAEVAAGSLFOGSPNMGRLVAFVFGAALCAESVNKEMEPLVGQVQEMWVAY 129  
QY 130 LETRLADWIHSSGGWAEFTALYDGALEEARRRREGNMAVSRVTLTGAVAGALVTYCAF 189  
DB 165 LETNLDRTIQSNGWNGFLTYDGAIEEARRRREGNMAVSRVTLTGAVAGALVTYCAF 189  
QY 190 FASK 193  
DB 225 FASK 228



```
RESULT 8
US-10-402-017-6
; Sequence 6, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to gen
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; PRIOR APPLICATION NUMBER: April 2, 2002
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del26-83)
US-10-402-017-6

Query Match          45.4%; Score 457.5; DB 15; Length 179;
Best Local Similarity 52.0%; Pred. No. 1.8e-39;
Matches 91; Conservative 21; Mismatches 56; Indels 7; Gaps 2;

QY 11 RALVADFGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRTFSDLAQLHV 70
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 6 RELVDFLSYKLSQKGYWSMAA-----AAAVKQALREAGDEFELRRRAFSDLTSQLHI 60

QY 71 TPGSAQGRFTQVSDLEFQGGPNWGRVAFVFGAALCAESVKNKEMBLVGQVQEMVAVYL 130
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 TPGTAVQSFQVNVNELFRDGVNMGRIYAFPSFGALCVESVDKEMQVLVSRIASWMATYL 120

QY 131 ETRLADWTHSSGGWAEFTALYGDGALBEARRLRE--GNWASVRTVLTGAVALGAL 183
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 NDHLEPWIQDNGGWDTFVELYGNNAAEBSRKQGERFNRWFLTGMTVAGVVLGSL 175

RESULT 9
US-10-402-017-8
; Sequence 8, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to gen
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; PRIOR APPLICATION NUMBER: April 2, 2002
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del46-83)
US-10-402-017-8

Query Match          44.5%; Score 448.5; DB 15; Length 199;
Best Local Similarity 47.9%; Pred. No. 1.8e-38;
Matches 91; Conservative 21; Mismatches 61; Indels 17; Gaps 2;

QY 11 RALVADFGYKLRQKGYV-----GAGPGEPAADPLHQAMRAAGDEFET 55
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 6 RELVDFLSYKLSQKGYWSQFSDVEENRTEAPEGTESERAAAAAAYKQALREAGDEFEL 65

QY 56 RFRRTFSDLAQLHVTGPSAQGRFTQVSDLEFQGGPNWGRVAFVFGAALCAESVNKEM 115
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DB 66 RYRRASFSDLTSQLHITPGTAVQSFQVNVNELFRDGVNMGRIYAFPSFGALCVESVDKEM 125

QY 116 EPLVGQVQEMVAVYLETRLADWTHSSGGWAEFTALYGDGALBEARRLRE--GNWASVRTV 173
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 126 QVLVSRIASWMATYLNHLEPWIQDNGGWDTFVELYGNNAAEBSRKQGERFNRWFLTGMT 185

QY 174 LTGAVALGAL 183
DB 186 VAGVVLGSL 195

RESULT 10
US-10-402-017-10
; Sequence 10, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to gen
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; PRIOR APPLICATION NUMBER: April 2, 2002
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del66-83)
US-10-402-017-10

Query Match          43.8%; Score 441.5; DB 15; Length 219;
Best Local Similarity 43.3%; Pred. No. 1.1e-37;
Matches 91; Conservative 21; Mismatches 61; Indels 37; Gaps 2;

QY 11 RALVADFGYKLRQKGYV-----CGAGPGE 35
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 6 RELVDFLSYKLSQKGYWSQFSDVEENRTEAPEGTESERETPSAINGNPSWHLADSPAV 65

QY 36 GPAADPLHQAMRAAGDEFETRFRRTFSDLAQLHVTGPSAQGRFTQVSDLEFQGGPNWGR 95
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 66 AAAAAYKQALREAGDEFELRYRRASFSDLTSQLHITPGTAVQSFQVNVNELFRDGVNMG 125

QY 96 LVAFVFGAALCAESVNKEMBLVGQVQEMVAVYLETRLADWTHSSGGWAEFTALYGDGA 155
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 126 IVAFFSFGALCVESVDKEMQVLVSRIASWMATYLNHLEPWIQDNGGWDTFVELYGNNA 185

QY 156 LBEARRLRE--GNWASVRTVLTGAVALGAL 183
DB 186 AAEBSRKQGERFNRWFLTGMTVAGVVLGSL 215

RESULT 11
US-10-402-017-12
; Sequence 12, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to gene
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; PRIOR APPLICATION NUMBER: April 2, 2002
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 219
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QY 29 CGAGPGEPPAD-----PLHQAMRAAGDEFFTRFRRTFSDLAAQLHVTGSAQQRFT 80  
DB 66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPTGTAYQSFE 124  
QY 81 QVSDLPFGGPNWGRIVAFVFGAALCAESVNKEMEPLVGQVQEMWVAYLETRLADWIHS 140  
DB 125 QVNNELFRDGVNWGRIVAFSFGALCVESVDKEMQVLVSRIASWMATYLNHLEPWIQD 184  
QY 141 SGWAEFTALYGDGALAEARLRE--GNWASVRTVLTGAVALLGAL 183  
DB 185 NGWDTFVELYGNNAALAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 15  
US-09-734-846-2  
; Sequence 2, Application US/09734846  
; Patent No. US20010007025A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Nikoloff, Brian J.  
; APPLICANT: Zhang, Qingqing  
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
; FILE REFERENCE: ISPH-0528  
; CURRENT APPLICATION NUMBER: US/09/734,846  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 09/277,020  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 09/167,921  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 09/323,743  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-734-846-2

Query Match 42.6%; Score 428.5; DB 9; Length 233;  
Best Local Similarity 40.6%; Pred. No. 2.8e-36;  
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;  
QY 11 RALVADPVGKLRQKGY-----VCGAGP-----GEGPAA 39  
DB 6 RELVVDPLSYKLSQKGYWSQFSDVEENRTAPEGTESEMETPSAINGNPSWHLADSPAV 65  
QY 40 D-----PLHQAMRAAGDEFFTRFRRTFSDLAAQLHVTGSAQQRFTQ 81  
DB 66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPTGTAYQSFEQ 125  
QY 82 VSDELFGGPNWGRIVAFVFGAALCAESVNKEMEPLVGQVQEMWVAYLETRLADWIHS 141  
DB 126 VVNNELFRDGVNWGRIVAFSFGALCVESVDKEMQVLVSRIASWMATYLNHLEPWIQEN 185  
QY 142 GGWAEFTALYGDGALAEARLRE--GNWASVRTVLTGAVALLGAL 183  
DB 186 GGWDTFVELYGNNAALAESRKQGERFNRWFLTGMTVAGVLLGSL 229

Search completed: April 10, 2005, 22:59:27  
Job time : 228.5 secs

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149056  
bcl-x long - mouse  
C:/Species: Mus musculus (house mouse)  
C:/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:/Accession: 149056; S52866  
R:/Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A:/Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
A:/Reference number: 149055; MUID:95052604; PMID:7963517  
A:/Accession: 149056  
A:/Status: preliminary; translated from GB/EMBL/DBJ  
A:/Molecule type: mRNA  
A:/Residues: 1-233 <RES>  
A:/Cross-references: UNIPROT:Q64373; EMBL:U10101; NID:g506647; PIDN:AAA82173.1; PID:g5066  
R:/Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.  
Submitted to the EMBL Data Library, November 1994  
A:/Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line throu  
A:/Reference number: S52866  
A:/Accession: S52866  
A:/Status: preliminary  
A:/Molecule type: mRNA  
A:/Residues: 1-233 <KAM>  
A:/Cross-references: EMBL:X83574; NID:g695622; PIDN:CAA58557.1; PID:g695623  
C:/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 42.6%; Score 428.5; DB 2; Length 233;  
Best Local Similarity 41.3%; Pred. No. 1.4e-32;  
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADFGVYKLRQKGY-----V 28  
DB 6 RELVVDFLSYKLSQKGYWSQFSVDEENRTAPEETEARETTPSAINGNPSWHLADSPAV 65  
QY 29 CGAGPGEPPAD-----PLHQMRAAGDEFEFRRTFSDLAQLHVTGPSAQQRFT 80  
DB 66 NGA-TGHSSSLDAREVTPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPTGTAYQSFE 124  
QY 81 QVSDLEFGGPNWGRLLVAFVFGAALCAESVNKEMEPLVGQVQEWVAVYLETRLADWTHS 140  
DB 125 QVAVNELFRDGVNMGRIVAFSFGALCVESVDKEMQVLVSRIASWMTATYLNHLEPWIQE 184  
QY 141 SGGWAEFTALYGDALEEARLRE--GNWASVRTVLTGAVALGAL 183  
DB 185 NGGWDTFVDLYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 3  
S51761  
BCL-X protein - rat

C:/Species: Rattus norvegicus (Norway rat)  
C:/Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C:/Accession: S51761; S51762  
R:/Michaelidis, T.M.  
Submitted to the EMBL Data Library, November 1994  
A:/Reference number: S51761  
A:/Accession: S51761  
A:/Status: preliminary  
A:/Molecule type: DNA  
A:/Residues: 1-233 <MIC>  
A:/Cross-references: UNIPROT:P53563; EMBL:X82537; NID:g607176; PIDN:CAA57886.1; PID:g6071  
A:/Experimental source: embryonic; brain  
A:/Accession: S51762  
A:/Status: preliminary  
A:/Molecule type: DNA  
A:/Residues: 1-125,189-233 <MI2>  
A:/Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57887.1; PID:g607178  
A:/Experimental source: embryonic; brain  
A:/Note: smaller form due to splicing  
C:/Genetics:  
A:/Introns: 125/3  
C:/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 42.2%; Score 424.5; DB 2; Length 233;

Best Local Similarity 41.3%; Pred. No. 3.4e-32;  
Matches 92; Conservative 22; Mismatches 56; Indels 53; Gaps 4;  
QY 13 LVADFGVYKLRQKGY-----VCG 30  
DB 8 LVVDLFSLYKLSQKGYWSQFSVDEENRTAPEETEARETTPSAINGNPSWHLADSPAVNG 67  
QY 31 AGPGEPPAD-----PLHQMRAAGDEFEFRRTFSDLAQLHVTGPSAQQRFTQV 82  
DB 68 A-TGHSSSLDAREVTPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPTGTAYQSFEQV 126  
QY 83 SDELFGGPNWGRLLVAFVFGAALCAESVNKEMEPLVGQVQEWVAVYLETRLADWTHSSG 142  
DB 127 VNELFRDGVNMGRIVAFSFGALCVESVDKEMQVLVSRIASWMTATYLNHLEPWIQENG 186  
QY 143 GWAFTALYGDALEEARLRE--GNWASVRTVLTGAVALGAL 183  
DB 187 GWDTFVDLYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 4  
A37332

transforming protein (bcl-2-alpha) - chicken  
C:/Species: Gallus gallus (chicken)  
C:/Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 09-Jul-2004  
C:/Accession: A37332; S35453  
R:/Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res. 20, 4187-4192, 1992  
A:/Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vari  
A:/Reference number: A37332; MUID:92375724; PMID:1508712  
A:/Accession: A37332  
A:/Status: nucleic acid sequence not shown  
A:/Molecule type: DNA  
A:/Residues: 1-233 <EGU>  
A:/Cross-references: UNIPROT:Q00709; EMBL:D11381  
C:/Genetics:  
A:/Introns: 189/3  
C:/Superfamily: bcl apoptosis regulator, inhibitory type  
C:/Keywords: mitochondrion; transforming protein; transmembrane protein

Query Match 42.1%; Score 423.5; DB 2; Length 233;  
Best Local Similarity 38.0%; Pred. No. 4.2e-32;  
Matches 87; Conservative 32; Mismatches 61; Indels 49; Gaps 4;

QY 9 DTRALVADFGVYKLRQKGYCGAG-----PGEPPADP----- 41  
DB 10 DNKEIVLKYIHYKLSQRGYDWAAGEDPRPPAPAPAAAPAAVAAAGASSHHRPEPPSA 69  
QY 42 -----LHQMRAAGDEFEFRRTFSDLAQLHVTGPSAQQRFTQVSD 84  
DB 70 AASEVPPAEGLRPAPPGVHLALRQAGDEFSSRRYQDFQMSQGLHTPTAHGRFAVVE 129  
QY 85 ELFGGPNWGRLLVAFVFGAALCAESVNKEMEPLVGQVQEWVAVYLETRLADWTHSSGW 144  
DB 130 ELFRDGVNMGRIVAFSFGALCVESVNREMSPLVDNIATWMTXYLNHNLHNIQDNGW 189  
QY 145 AEFTALYGDALEEARLREGNWSVRTVLTGAVALGALVTGAFASK 193  
DB 190 DAFVELYGN---SMRPLPFRSWSLSKLTLS-LVVGACITLIGAYLGHK 233

RESULT 5  
S24390

transforming protein (Bcl-2) homolog - chicken  
C:/Species: Gallus gallus (chicken)  
C:/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:/Accession: S24390  
R:/Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.  
Biochim. Biophys. Acta 1132, 109-113, 1992  
A:/Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue  
A:/Reference number: S24390; MUID:92379084; PMID:1511008  
A:/Accession: S24390  
A:/Status: preliminary



## RESULT 8

153744

gene bcl-2 protein - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004

C/Accession: 153744

R/Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.

Gene 140, 291-292, 1994

A/Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.  
A/Reference number: 153744; MUID:94193015; PMID:8144041

A/Accession: 153744

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-236 &lt;RES&gt;

A/Cross-references: UNIPROT:P49950; GB:L14680; NID:g408946; PIDN:AAA53662.1; PID:g408947

A/Genetics:

A/Gene: bcl-2

C/Superfamily: bcl apoptosis regulator, inhibitory type

## Query Match

Best Local Similarity 40.4%; Score 407; DB 2; Length 236;

Matches 83; Conservative 34; Mismatches 63; Indels 52; Gaps 3;

QY 9 DTRALVADFGYKLRQKGY-----PG----- 27

Db 10 DNREIVMKYIHYKLSQRGYEMDTGDEDSAPLRAAPTFGIFSFPESNRPVAVHRDART 69

QY 28 -----VCGAGPGEPRADPLHQAMRAAGDEFETRFRRTFSDLAQLHVTGPSAQQRFTQ 81

Db 70 SPLRPLVANAGPALSPVPEVVHLLTRRAGDPSRRYRDFAEISSQLHLTPFTARGRFAT 129

QY 82 VSDELFOGGPNMGRVAFVFGAALCAESVKNKMEPLVGVQVQEWNVAYLETRLADWIHSS 141

Db 130 VVEELFRDGVNMGRIVAFEFEGVCMCVSVNREMSPLVDNIALMTEYLNRHLHTWIQDN 189

QY 142 GGMWAEFTALYGDCALAEARRLREGNMAVSVTVLTGAVALGALVTGAFPAASK 193

Db 190 GGMWDAFVELYG-----PSMRPLFDPSWLSLKTLLS-LPVGACITLGAVALGHK 236

## RESULT 9

TVMSA1

transforming protein bcl-2-alpha - mouse

C/Species: Mus musculus (house mouse)

C/Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 28-Jul-2003

C/Accession: A25960; E37332

R/Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.

Cell 49, 455-463, 1987

A/Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homolog  
A/Reference number: A90893; MUID:87187643; PMID:3032455

A/Accession: A25960

A/Molecule type: DNA

A/Residues: 1-236 &lt;NEG&gt;

A/Cross-references: GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1; PID:g387109

R/Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A/Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety  
A/Reference number: A37332; MUID:92375724; PMID:1508712

A/Accession: E37332

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A/Molecule type: DNA

A/Residues: 1-33, 'E', 34-220, 'AL', 223-236 &lt;EGU&gt;

A/Genetics:

A/Gene: BCL2

A/Introns: 192/3

C/Superfamily: bcl apoptosis regulator, inhibitory type

C/Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane pro

## Query Match

Best Local Similarity 40.3%; Score 406; DB 1; Length 236;

Matches 86; Conservative 33; Mismatches 61; Indels 52; Gaps 5;

QY 9 DTRALVADFGYKLRQKGYCGAG-----PG----- 34  
Db 10 DNREIVMKYIHYKLSQRGYEMDAGDADAAPLGAAPTFGIFSFPESNMPAVHREMAART 69  
QY 35 -----EGPADP-----LHQAMRAAGDEFETRFRRTFSDLAQLHVTGPSAQQRFTQ 81  
Db 70 SPLRPLVATAGPALSPVPEVCVHLLTRRAGDPSRRYRDFAEISSQLHLTPFTARGRFAT 129  
QY 82 VSDELFOGGPNMGRVAFVFGAALCAESVKNKMEPLVGVQVQEWNVAYLETRLADWIHSS 141  
Db 130 VVEELFRDGVNMGRIVAFEFEGVCMCVSVNREMSPLVDNIALMTEYLNRHLHTWIQDN 189  
QY 142 GGMWAEFTALYGDCALAEARRLREGNMAVSVTVLTGAVALGALVTGAFPAASK 193  
Db 190 GGMWDAFVELYG-----PSMRPLFDPSWLSLKTLLS-LPVGACITLGAVALGHK 236

## RESULT 10

167431

BCL-X-Long - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004

C/Accession: 167431

R/Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.

A/Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equine  
onstitutive bcl-2 and bcl-x-long messenger ribonucleic acid levels.

A/Reference number: 153295; MUID:95129487; PMID:7828536

A/Accession: 167431

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-233 &lt;RES&gt;

A/Cross-references: UNIPROT:P53563; EMBL:U34963; NID:g1004376; PIDN:AAA77686.1; PID:g1004

C/Superfamily: bcl apoptosis regulator, inhibitory type

## Query Match

Best Local Similarity 40.2%; Score 404.5; DB 2; Length 233;

Matches 89; Conservative 22; Mismatches 61; Indels 53; Gaps 4;

QY 11 RALVADFGYKLRQKGY-----V----- 28

Db 6 RELVDFLSYKLSQKGYNSQFSDVEENRTAEETPERETPSAINGNPSWHLADSPAV 65

QY 29 CGAGPGEPRAD-----PLHQAMRAAGDEFETRFRRTFSDLAQLHVTGPSAQQRFT 80

Db 66 NGA-TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPGTYQSF 124

QY 81 QVSDELFOGGPNMGRVAFVFGAALCAESVKNKMEPLVGVQVQEWNVAYLETRLADWIHSS 140

Db 125 QVNNELFRDGVNMGRIVASSFGALCVESVDKEMQVLVSRIASWMTATYLNHLEPWIOE 184

QY 141 SGMWAEFTALYGDCALAEARRLREGNMAVSVTVLTGAVALGAL 183

Db 185 NGMWDTFVDLYGNNTAPBSRKQGERFNRWFLTGMTVAGVLLGSL 229

## RESULT 11

JC7383

B-cell lymphoma 2 protein - Chinese hamster

C/Species: Cricetus griseus (Chinese hamster)

C/Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 09-Jul-2004

C/Accession: JC7383

R/Tomicic, M.T.; Christmann, M.; Kaina, B.

Biochem. Biophys. Res. Commun. 275, 899-903, 2000

A/Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.  
A/Reference number: JC7383

A/Contents: Ovary

A/Accession: JC7383

A/Molecule type: mRNA

A/Residues: 1-236 &lt;TOM&gt;

A/Cross-references: UNIPROT:Q9JUV8; GB:AJ271720

C/Comment: This protein has anti-apoptotic function, and supports cell survival.



C;Genetics:  
A;Gene: bcl-2  
C;Superfamily: bcl apoptosis regulator, inhibitory type  
C;Keywords: B-cell lymphoma; ovary

Query Match	40.0%;	Score 403;	DB 2;	Length 236;
Best Local Similarity	35.3%;	Pred. No. 3.5e-30;		
Matches 82;	Conservative 34;	Mismatches 64;	Indels 52;	Gaps 3;

```

QY      9 DTRALVADPVGYKLRQKGY----- 27
      | | : : | | : | |
Db     10 DNREIWMKYIHKL$QRGYEMWDVGDVDAPLGAAFTPGIFS$QPE$NPTPAVHRDMAART 69
QY     28 -----VCGAGPGE$GPAADPLHQAMRACGDEFETRFRRTFSDLAQLHTVTPGSAOQRFTQ 81
      | | | | : : | | : | | : | | : | | : | | : | |
Db     70 SPLRPIVATTGFTLSPVPFPVWHLLTRRAGDDFSRRYRDFAE$MSQLHTLTPFARGRFAT 129
QY     82 V$DELFQCG$P$NMWGRLVAFVFGALCAESY$NKEMEPLVGQVQ$EMWVAYLETRLADWIIHS 141
      | : | | : | | | | | | | : | | | | | | | : | | | | :
Db     130 V$EELFRDGVNMGRIVAFEF$FGV$C$VESY$NRE$MSPLVDNIALMTEYLRNRLHTWIQDN 189
QY     142 G$WAEFTALYGDGALBEARRLREG$N$WASV$RTVL$TGAVALGALVTVGAF$PASK 193
      | | | | | | | : : : | | : | | : | | : | |
Db     190 G$WDAF$VELY$---P$VRPLFDF$WLSL$KTLILSLAL-VGACITLGTLYLGHK 236

```

RESULT 12  
A47537  
apoptosis regulator bcl-x - chicken  
C/Species: Gallus gallus (chicken)  
C/Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004  
C/Accession: A47537  
R/Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;  
Cell 74, 597-608, 1993  
A/Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic  
A/Reference number: A47537; MUID:93364977; PMID:8358789  
A/Accession: A47537  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-190 <BOI>  
A/Cross-references: UNIPROT:Q07816; GB:Z23110; GB:I20120; NID:G510898; PIDN:CAA80657.1;  
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match	37.5%	Score 378	DB 2	Length 190
Best Local Similarity	43.8%	Pred. No. 5.9e-28		
Matches	81	Conservative 14	Mismatches 44	Indels 46
				Gaps 3
QY	11 RALVADFVGKYLRQKGY-----VCGAGPGEGP-----	37		
	:			
Db	6 RELVIDFVSYKLSQRGHCMSELEBEDENRTDTAAEAEMDSVLNGSPSMHPPAGHVNGAT	65		
QY	38 -----AADPLHQAMRAAGDEFETRFRRTFSDLAQLHTVTPGSAQQRFTQVSD	85		
	:     :                                 :			
Db	66 VHRSSLEVHEIVRASDVRRQLRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVANE	125		
QY	86 LFQGGPNMGRLVAFVFFGALCAESVYNKEMEPVLGVQVQDENNVAVYLETRLADWIHSSGNA	145		
	:			
Db	126 LFHDGVNMGRIVAFFSFGALCVESVDKEMRVLVGRIVSMWTTYLLTDHLDPMIQENGWV	185		
QY	146 EFTAL 150			
Db	186 R-TAL 189			

RESULT 13  
I49057  
bcl-x transmembrane deleted - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I49057  
R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.

A;Reference number: I49055; MUID:95052604; PMID:7963517  
A;Accession: I49057  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-214 <RES>  
A;Cross-references: UNIPROT:Q64373; EMBL:U10102; NID:G506649; PIDN:AAA82174.1; PID:G50665  
C;Genetics:  
A;Gene: bcl-x-long  
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match	37.5%;	Score 377.5;	DB 2;	Length 214;
Best Local Similarity	42.8%;	Pred. No. 7.6e-28;		
Matches	80;	Conservative	16;	Mismatches 40;
				Indels 51;
				Gaps 3;

```

QY      11 RALVADFVGKLRQKGY-----V 28
      || ||: ||| |||
Db      6 RELVVDFLSYKLSQKGYSWGQSDVEENRTEAPEETEARETTPSAINGNPSWHLADSPAV 65
QY      29 CGAGPGEGPAD-----PLHQAMRAAGDEFEFTRFRRTFSDLAOLHYTPGSAQQRFT 80
      || | : | : ||: ||||| : || ||| : |||: |||: ||
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPGTAYQSFE 124
QY      81 QVSDLEFQGGPNMGRVLVAFVFGALCAESVNKEMEPLVGQVQENMVAYLETRLADWIHS 140
      ||: |||: |||: |||: ||| ||| |||: |||: ||: || || ||
Db      125 QVNNELFRDGVNMGRIVAFPSFGGALCVESVDKEMQVLVSRIASNMATYLNDRLEPWIQE 184
QY      141 SGGWAEF 147
      : ||| |
Db      185 NGGWDTF 191

```

RESULT 14  
JE0203  
apoptosis regulator bcl-x isoform - human  
N;Alternate names: h-bcl-xbeta  
C/Species: Homo sapiens (man)  
C/Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 09-Jul-2004  
C/Accession: JE0203  
R;Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler, E.  
Biochem. Biophys. Res. Commun. 248, 147-152, 1998  
A/Title: Identification of a human cDNA encoding a novel bcl-x isoform.  
A/Reference number: JE0203; MUID:98340865; PMID:9675101  
A/Accession: JE0203  
A/Molecule type: mRNA  
A/Residues: 1-227 <BAN>  
A/Cross-references: UNIPROT:Q07817; GB:U72398; NID:g1622940; PIDN:AAB17354.1; PID:g1622940  
C/Genetics:  
A/Gene: bcl-x  
A/Map position: 20  
C/Superfamily: bcl apoptosis regulator, inhibitory type

```

Query Match      37.3%; Score 375.5; DB 2; Length 227;
Best Local Similarity 40.8%; Pred. No. 1.3e-27;
Matches 82; Conservative 18; Mismatches 50; Indels 51; Gaps 3;

QY      11 RALVADFVGKYKLROKGY-----Y 28
      |||::||| |||
Db       6 RELVDFLSYKLSQKGYSMSQFSDVEENRTEAPEGTSEMETPSALINGNPSWHLADSPAV 65
      |||::||| |||

QY      29 CGAGPGEGRPAD-----PLHQAMRAAGDEFETRFRRTFSDLAQLHTVPGSAQGRFT 80
      |||::||| :|||::||| |||::||| |||::||| |||

Db       66 NGA-TGHSSSLDAREVI PMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPGTAYQSFE 124
      |||::||| :|||::||| |||::||| |||::||| |||

QY      81 QVSDelfOGGPNMGRVLVAFVFGALCAESVNKEMPLVGQVQVEWMVAYLETRLADWTHS 140
      |||::||| :|||::||| |||::||| |||::||| |||::||| |||

Db      125 QVNNELFRDGVNMGRIVAFFSFGALCVESVDKEMQVLVSRIAAWMATYLLNDHLEPWIOE 184
      |||::||| :|||::||| |||::||| |||::||| |||

QY      141 SGGWAEFTALYGDGALBEARR 161
      :|||::||| :|||::|||

Db      185 NGGWRTKPLVCPFSLASGQR 205
      :|||::||| :|||::|||

```

## RESULT 15

**B37332**

transforming protein (bcl-2-beta) - chicken

C;Species: Gallus gallus (chicken)

```
C:\Date: 03-Mar-1993 #sequence_ 03-Mar-1993 #text_change 28-Jul-2003
```

C/Accession: B37332; S35452

R; Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A; Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie

A:Reference number: A37332; MUID:92375724; PMID:1508712

A;Accession: B37332

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-216 <EGU>

A/Cross-references: EMBL:D11381; EMBL:D11382

C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match	35.4%	Score 356;	DB 2;	Length 216;
Best Local Similarity	38.4%;	Pred. No. 7.8e-26;		
Matches 71; Conservative	21;	Mismatches 49;	Indels 44;	Gaps 22;

QY 9 DTRALVADFVGYYLRQKGYVCGAG-----PGEGRPADP----- 41

Db 10 D N R E I V L K Y I H Y K L S Q R G Y D W A A G E D R P P V P P A P A P A A P A A V A A A G A S S H R P E P P G S A 69

QY 42 -----LHQAMRAAGDEFETRFRRTFSDLAOLHVT PGSAOORFTOVSD 84

Db 70 AASEVPAEGLRPAPGVHLALROAGDEFSRRYORDEAOMSGOLHTPTAGRFVAVVE 129

85 ELFOGCPNWGR LVAFVEFGALCAESVNKEMEPLVGVOEWMVAYIETRIADWTHSSGGW 144

Db 130 ELFRDGVNMGRIVAFFEEFGVMCVESVNBREMSPLVDNIAATWMTET.NRHI.HNWITODNGCW 199

QY 145 AEF7A 149

Db 190 VRACA 194

Search completed: April 10, 2005, 22:44:41  
Job time : 19 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 14:45:43 ; Search time 3057.74 Seconds  
(without alignments)  
9206.966 Million cell updates/sec

Title: US-09-925-674B-8

Perfect score: 581  
Sequence: 1 atgcgcgaccccgacctcaac.....gccttttctgctagaagtg 581

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_da:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_srs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	581	100.0	581	6 AX022531	AX022531 Sequence
2	581	100.0	581	6 AX030819	AX030819 Sequence
3	560.2	96.4	582	10 MMUS9746	US9746 Mus musculu
4	560.2	96.4	3476	10 AF030769	AF030769 Mus muscu
5	549.2	94.5	3442	10 AK172925	AK172925 Mus muscu
6	544.2	93.7	582	10 AF096291	AF096291 Rattus no
7	544.2	93.7	1110	10 AY185100	AY185100 Rattus no
8	544.2	93.7	3487	10 AY185098	AY185098 Rattus no
9	544.2	93.7	3545	10 BC074021	BC074021 Rattus no
10	541	93.1	3473	10 AY170344	AY170344 Mus muscu
11	540.6	93.0	579	6 AR020779	AR020779 Sequence
12	505.8	87.1	582	6 AX481423	AX481423 Sequence
13	505.8	87.1	582	9 HSUS9747	US9747 Homo Bcl-w
14	502.6	86.5	3542	9 D87461	D87461 Homo sapien
15	501	86.2	582	6 CQ730429	CQ730429 Sequence
16	501	86.2	583	6 AX022529	AX022529 Sequence
17	501	86.2	583	6 AX030817	AX030817 Sequence
18	497.4	85.6	579	6 AR020780	AR020780 Sequence
19	451.4	77.7	220818	2 AC128940	AC128940 Rattus no

20	451.4	77.7	223933	2 AC097389	AC097389 Rattus no
21	421.8	72.6	3815	10 BC040369	BC040369 Mus muscu
22	421.8	72.6	237561	10 AC116591	AC116591 Mus muscu
23	407.4	70.1	210784	2 AC119293	AC119293 Rattus no
24	407.4	70.1	263901	2 AC115371	AC115371 Rattus no
25	390.8	67.3	148278	2 AC079885	AC079885 Rattus no
26	390.8	67.3	180665	2 AC084240	AC084240 Rattus no
27	390.8	67.3	221557	2 AC134055	AC134055 Rattus no
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35	232.6	40.0	1053	5 BC073259	BC073259 Xenopus 1
36	232.6	40.0	1894	5 BC084445	BC084445 Xenopus t
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38	191	32.9	6049	6 AX345131	AX345131 Sequence
39	142.4	24.5	1252	4 AB073983	AB073983 Canis fam
40	140.8	24.2	1163	4 AB080951	AB080951 Felis cat
41	140.4	24.2	660	6 AX925694	AX925694 Sequence
42	139.6	24.0	540	6 AX925690	AX925690 Sequence
43	139.4	24.0	600	6 AX925692	AX925692 Sequence
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45	138.2	23.8	1184	5 GGU26645	U26645 Gallus gall

ALIGNMENTS

RESULT 1	AX022531	581 bp	DNA	linear	PAT 07-SEP-2000
LOCUS	AX022531	Sequence 8 from Patent EP0932674.			
DEFINITION	AX022531				
ACCESSION	AX022531	GI:10046127			
VERSION	AX022531.1				
KEYWORDS	unidentified				
SOURCE	unclassified				
ORGANISM	unclassified				
REFERENCE	1	Adams, J.M., Holmgren, S.P., Cory, S. and Gibson, L.M.			
AUTHORS		A novel mammalian gene, bcl-w, belongs to the bcl-2 family of			
TITLE		apoptosis-controlling genes			
JOURNAL		Patent: EP 0932674-A 8 04-AUG-1999;			
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Query Match	100.0%	Score 581;	DB 6;	Length 581;	
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Db 121 CCGCTGACCAAGCCATGCGGGCTGTGAGACGAGTTTGAGACCCGTTTCCGCCGACC 180  
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QY 241 CAGGTTCCGACGAATTTTCCAGAGGGGCCCTTAAGTGGGCGCTTGTGCAATCTTT 300  
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QY 541 GGGGCGCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTG 581  
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LOCUS AX030819 581 bp DNA linear PAT 20-SEP-2000  
DEFINITION Sequence 8 from Patent WO9735971.  
ACCESSION AX030819  
VERSION AX030819.1 GI:10278313  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.  
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of  
JOURNAL apoptosis-controlling genes  
ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU)  
; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)  
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Location/Qualifiers  
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ORIGIN

Query Match 100.0%; Score 581; DB 6; Length 581;  
Best Local Similarity 100.0%; Pred. No. 9.9e-126;  
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RESULT 3  
LOCUS MMU59746 582 bp mRNA linear ROD 29-SEP-1996  
DEFINITION Mus musculus Bcl-w (bcl-w) mRNA, complete cds.  
ACCESSION U59746  
VERSION U59746.1 GI:1572494  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
JOURNAL 1 (bases 1 to 582)  
ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; BAKER, E.; ADAMS, J.M. and CORY, S.  
; GIBSON, L.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S.  
bcl-w, a novel member of the bcl-2 family, promotes cell survival  
Oncogene 13 (4), 665-675 (1996)  
PUBMED 96358615  
MEDLINE 8761287  
REFERENCE 2 (bases 1 to 582)  
AUTHORS Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and  
Cory, S.  
TITLE Direct Submission  
JOURNAL Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and  
Eliza Hall Institute of Medical Research, PO Royal Melbourne  
Hospital, Parkville, Victoria 3050, Australia  
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Query Match 96.4%; Score 560.2; DB 10; Length 582;  
Best Local Similarity 97.8%; Pred. No. 7.5e-121;  
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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61 AAGCTGAGGAGAGAGGTTATGTCTGTGAGAGCTGGGCGCTGGGGAAGGCCAGCCGCGAC 120	
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RESULT 4  
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LOCUS AF030769  
DEFINITION Mus musculus BCL-W (Bcl-w) mRNA, complete cds.  
ACCESSION AF030769  
VERSION AF030769.1 GI:2623249  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 3476)  
AUTHORS Ross,A.J., Waymire,K.G., Moss,J.E., Parlow,A.F., Russell,L.D. and  
MacGregor,G.R.

TITLE Bcl-w is required for testis homeostasis  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3476)  
AUTHORS Ross,A.J. and MacGregor,G.R.  
TITLE Direct Submission  
JOURNAL Submitted (21-OCT-1997) Center for Molecular Medicine, Emory  
University, 1462 Clifton Road, Atlanta, GA 30322, USA

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Best Local Similarity 97.8%; Pred. No. 5.6e-121;  
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OY 1 ATGCCGACCCAGCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
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Db

OY 361 CAAGTCCAGGATGGATCGTGGCCCTACCTGAGACACGCTTGCTGATGATCCACAGC 420  
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RESULT 5  
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LOCUS  
DEFINITION Mus musculus mRNA for mKIAA0271 protein. linear ROD 28-JUL-2004  
ACCESSION AKI72925  
VERSION AKI72925.1 GI:50510434  
KEYWORDS FLI\_CDNA.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS Okazaki, N., Kikuno, R.F., Ohara, R., Inamoto, S., Koseki, H., Hiraoka, S., Saga, Y., Seino, S., Nishimura, M., Katsuno, T., Hoshino, K., Kitamura, H., Nagase, T., Ohara, O. and Koga, H.  
TITLE Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene: IV. The Complete Nucleotide Sequences of 500 Mouse of KIAA-Homologous cDNAs Identified by Screening of Terminal Sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries  
JOURNAL DNA Res. 11, 205-218 (2004)  
REFERENCE  
AUTHORS Okazaki, N., Kikuno, R.F., Nagase, T., Ohara, O. and Koga, H.  
TITLE Direct Submission  
JOURNAL Submitted (19-MAY-2004) Hisashi Koga, Kazusa DNA Research Institute, Laboratory for Genome Informatics, 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan  
COMMENT The CREATE program supported by Japan science and technology corporation; cDNA full insert sequencing; Kazusa DNA Research Institute; cDNA library construction, clone selection and 5'- & 3'-end one pass sequencing.  
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Query Match 94.5%; Score 549.2; DB 10; Length 3442;  
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DB 66 AAGCTGAGGACAGAGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGCCGCGAC 120  
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DB 126 CCGCTGACCAAGCCATGCGGGCTGTGAGAGACGAGTTGAGACCCGTTCCGCGCAC 180  
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DB 546 GGGGCGGCTGGTAACTGTAGGGGCTTTTGT 575

RESULT 6  
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LOCUS  
DEFINITION Rattus norvegicus Bcl-1 (bcl-1) mRNA, complete cds.  
ACCESSION AF096291  
VERSION AF096291.1 GI:3747129  
KEYWORDS  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE  
AUTHORS Hamner, S., Skoglosa, Y. and Lindholm, D.  
TITLE Differential expression of bcl-1 and bcl-2 messenger RNA in the developing and adult rat nervous system  
JOURNAL Neuroscience 91 (2), 673-684 (1999)  
REFERENCE  
AUTHORS Hamner, S., Skoglosa, Y. and Lindholm, D.  
TITLE Direct Submission  
JOURNAL Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala University, Box 587, BMC, Uppsala 751 23, Sweden  
FEATURES  
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Sciurognathi;
Rodentia; Chordata; Eutheria; Mammalia;
Eukaryota; Metazoa;
Rattus.
1 (bases 1 to 1110) expression during
Itoh,T., Itoh,A. and Pleasure,D.
Bcl-2-related protein family gene differentiation
oligodendroglial (2003)
J. Neurochem. 85 (6), 1500-1512
22672518
JOURNAL MEDLINE PUBMED
12787069
2 (bases 1 to 1110)
Itoh,T., Itoh,A. and Pleasure,D.
Direct Submission Research, The Children's Hospital
Submitted (21-NOV-2002) Neurology Center 516 I, 3517 Civic Center
of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center
Blvd., Philadelphia, PA 19104, USA
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ORIGIN	Query Match	Similarity	Score	DB	Length	Indels	Gaps
Best local Matches	558;	Conservative	93.7%; 96.0%;	Pred. No. 0;	Mismatches 23;		
QY	1	ATGCCGACCCCGAGCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTGTAGGCTAT	60				
Db	509	ATGGCGACCCCGAGCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTGTAGGCTAT	568				
QY	61	AGGCTGAGCGAGAGGGTTATGTCGTGTGAGCTGGCCCTTGGGGAAGGCCCAAGCCCGAC	120				
Db	569	AACTGAGGCGAGAGGGTTATGTCGTGTGAGCTGGCCCTTGGGGAAGGCCCAAGCCCGAC	628				
QY	121	CCGCTGACCAAGCCATGCGGCTGTGTGAGACAGAGTTTGAACCCGTTTCCGCGCCACC	180				
Db	629	CCGCTGACCAAGCCATGCGGCTGTGTGAGACAGAGTTTGAACCCGTTTCCGCGCCACC	688				
QY	181	TTCTCTGACCTGGCCGCTGAGCTAACAGTGACCCCAAGGCTCAGCCAGCAACGCTTACC	240				
Db	689	TTCTCTGACCTGGCCGCTGAGCTAACAGTGACCCCAAGGCTCAGCCAGCAACGCTTACC	748				
QY	241	CAGGTTTCCGACGAACTTTTCCAGGGGGCCCTTAATCTGGGGCCGTCTTGTGGCAATCTTT	300				
Db	749	CAGGTTTCCGACGAACTTTTCCAGGGGGCCCTTAATCTGGGGCCGTCTTGTGGCAATCTTT	808				
QY	301	GTCCTTGGGGCTGCCCTGTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCATTGTGGGA	360				
Db	809	GTCCTTGGGGCTGCCCTGTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCATTGTGGGA	868				
QY	361	CAAGTCCAGGATTTGATCGTGGCTTAACCTGAGAGACGCTTGGCTGACTGATCCACAGC	420				
Db	869	CAAGTCCAGGATTTGATCGTGGCTTAACCTGAGAGACGCTTGGCTGACTGATCCACAGC	928				
QY	421	AGTGCGGCTGGCGGACTTACAGCTCTTAACGGGACGGGCCCTTGAGAGACGACGCG	480				
Db	929	AGTGCGGCTGGCGGACTTACAGCTCTTAACGGGACGGGCCCTTGAGAGACGACGCG	988				
QY	481	CGTCTGCGGAGGAGGCACTGGGCAATGAGACAGTGTGACGGGGCTGTGCACTG	540				
Db	989	CGTCTGCGGAGGAGGCACTGGGCAATGAGACAGTGTGACGGGGCTGTGCACTG	1048				



REMARK COMMENT
<p>USA, National Institutes of Health, Mammalian            NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>            Contact: MGC help desk            Email: <a href="mailto:cgabbs@mail.nih.gov">cgabbs@mail.nih.gov</a>            Tissue Procurement: Howard Jacobs            CDNA Library Preparation: Express            DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium            Gaithersburg Center (NISC),            Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a>            Contact: <a href="mailto:nisc_mgc@nhgri.nih.gov">nisc_mgc@nhgri.nih.gov</a></p>



Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,  
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,  
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,  
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Lalic,P., Legaspi,R.,  
Maduro,O.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,  
McDowell,J., Pearson,R., Staniripop,S., Thomas,P.J., Touchman,J.W.,  
Taurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,  
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>  
Series: IRAX Plate: 175 Row: p Column: 4  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 11177885.

FEATURES

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CDS

ORIGIN

Query Match 93.7%; Score 544.2; DB 10; Length 3545;  
Best Local Similarity 96.0%; Pred. No. 3.2e-117;  
Matches 558; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

OY 1 ATGCCGACCCAGCCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
Db 199 ATGGCGACCCAGCCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 258  
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Db 259 AAGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGGCTGGGAAGGCCAGCGAC 318  
OY 121 CCGCTGACCAAGCCATGCGGGCTGTGAGACAGATTGAGACCCGTTCCGCCGAC 180  
Db 319 CCGTGACCAAGCCATGCGGGCAGCTGAGACAGATTGAGACCCGCTCCGCCGAC 378  
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Db 439 CAGGTTCCGACGACTTTTCCAAGGGGGCCCTTAAGTGGGCGGCTTGTGGCAATCTTT 498  
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Db 499 GTCTTTGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGAGCCATTTGTGGGA 558  
OY 361 CAAGTCCAGATTGATCGTGGCTTACCTGAGACAGCTCTGGCTGATGATCCACAGC 420  
Db 559 CAAGTCCAGATTGATCGTGGCTTACCTGAGACAGCTCTGGCTGATGATCCACAGC 618  
OY 421 AGTGGCGGCTGGCGGACTTACAGCTCTATACGGGGAAGGGGCGCTGAGAGCGCACGG 480  
Db 619 AGTGGGCGCTGGCGGAGTTCAAGCTCTATACGGGGAAGGGGCGCTGAGAGCGCACGG 678  
OY 481 CGTCTGGGGAAGGCACTGGGCTAGTGAAGCAGTGTGACGGGGCGGTGGCACTG 540

Db 679 CGTCTGGGGAAGGCACTGGGCTAGTGAAGCAGTGTGACGGGGCGGTGGCACTG 738  
OY 541 GGGGCCCTGGTAAGTGTAGGGGCGCTTTTGTCTAGCAAGTG 581  
Db 739 GGGGCCCTGGTAAGTGTAGGGGCGCTTTTGTCTAGCAAGTG 779

RESULT 10

AY170344 3473 bp mRNA linear ROD 27-JAN-2004  
LOCUS Mus musculus Bcl2-like protein 2 mRNA, complete cds.  
DEFINITION AY170344  
ACCESSION AY170344  
VERSION AY170344.2 GI:34857712  
KEYWORDS

SOURCE

Mus musculus (house mouse)  
Mus musculus

REFERENCE

1 (bases 1 to 3473)  
Su,H.-Y., Cheng,W.T.K., Chen,S.C., Lin,C.T., Lien,Y.Y., Liu,H.J.  
and Gilmour,R.S.

TITLE

Mouse keratinocytes express c98, a novel gene homologous to bcl-2,  
that is stimulated by insulin-like growth factor 1 and prevents  
dexamethasone-induced apoptosis  
Biochim. Biophys. Acta 1676 (2), 127-137 (2004)

REFERENCE

2 (bases 1 to 3473)  
Su,H.-Y.

REFERENCE

Direct Submission  
Submitted (29-OCT-2002) Biotechnology, Pingtung University, No. 1,  
Hsueh Fu Road, Nei-Pu Hsiang, Pingtung, Taiwan 912, Taiwan  
3 (bases 1 to 3473)  
Su,H.-Y.

TITLE

Direct Submission  
Submitted (22-SEP-2003) Biotechnology, Pingtung University, No. 1,  
Hsueh Fu Road, Nei-Pu Hsiang, Pingtung, Taiwan 912, Taiwan

JOURNAL

Sequence update by submitter  
On Sep 22, 2003 this sequence version replaced gi:27497698.

REMARK

Location/Qualifiers  
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FEATURES

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CDS

OY 61 AGGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGCGCGAC 120  
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OY 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGCAGATTGAGACCCGTTCCGCCGAC 180  
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ORIGIN

Query Match 93.1%; Score 541; DB 10; Length 3473;  
Best Local Similarity 95.7%; Pred. No. 1.8e-116;  
Matches 556; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 1 ATGCCGACCCAGCCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
Db 182 ATGGCGACCCAGCCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 241  
OY 61 AGGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGCGCGAC 120  
Db 242 CAGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGCGCGAC 301  
OY 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGCAGATTGAGACCCGTTCCGCCGAC 180  
Db 302 CCGCTGACCAAGCCATGCGGCTGTGAGAGCAGATTGAGACCCGTTCCGCCGAC 361

QY 181 TTCTTGACCTGGCCGCTCAGCTACACGTGACCCCAAGGCTCAGCCCAAGCAACGCTTCACC 240  
Db 362 TTCTTCACTTGCCCGCTCAGCTACACGTGACCCCAAGGCTCAGCCCAAGCAACGCTTCACC 421  
QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGCGCTTAACTGGGGCGCTTGTGGCATTTCTTT 300  
Db 422 CAGGTTTCCGACGAACTTTTCCAAAGGGGCGCTTAACTGGGGCGCTTGTGGCATTTCTTT 481  
QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCACAAAGAAATGAGCCTTTGGTGGGA 360  
Db 482 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCACAAACATATGAGCCTTTGGTGGGA 541  
QY 361 CAAGTCCAGGATTGATCGTGGCCCTTACCTTGAGACACGCTCTGCTGACTGGATCCACAGC 420  
Db 542 CAAGTCCAGGATTGATCGTGGCCCTTACCTTGAGACACGCTCTGCTGACTGGATCCACAGC 601  
QY 421 AGTGGCGGCTGGCGGCACTTCAACAGCTCTATACGGGACGGGGCGCTTGAGAGACGACGG 480  
Db 602 AGTGGCGGCTGGCGGCACTTCAACAGCTCTATACGGGACGGGGCGCTTGAGAGACGACGG 661  
QY 481 CGTCTGCGGAGGGCAACTGGGCATGATGAGACACAGTGTGACGGGGCGCTGGCACTG 540  
Db 662 CGTCTGCGGAGGGCAACTGGGCATGATGAGAGACAGTGTGACGGGGCGCTGGCACTG 721  
QY 541 GGGGCCCTGGTAACTGTAGGGGCGCTTTTGTCTAGCAAGTG 581  
Db 722 GGGGCCCTGGTAACTGTAGGGGCGCTTTTGTCTAGCAAGTG 762

RESULT 11  
LOCUS AR020779 579 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 1 from patent US 5789201.  
ACCESSION AR020779  
VERSION AR020779.1 GI:3975394  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 579)  
TITLE Guastella,J.  
JOURNAL Genes coding for bcl-1 and bcl-2 homologue  
FEATURES Patent: US 5789201-A 1 04-AUG-1998;  
location/Qualifiers  
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ORIGIN

Query Match 93.0%; Score 540.6; DB 6; Length 579;  
Best Local Similarity 95.9%; Pred. No. 3e-116;  
Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGGCTTCAACCCCAAGACACACGCGCTTGTGGCTGACTTTGTAGGCTAT 60  
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QY 61 AGGCTGAGGCAAGAGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGCCGCGGAC 120  
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QY 181 TTCTTGACCTGGCCGCTCAGCTACACGTGACCCCAAGGCTCAGCCCAAGCAACGCTTCACC 240  
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QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGCGCTTAACTGGGGCGCTTGTGGCATTTCTTT 300  
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QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCACAAAGAAATGAGCCTTTGGTGGGA 360  
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QY 361 CAAGTCCAGGATTGATCGTGGCCCTTACCTTGAGACACGCTCTGCTGACTGGATCCACAGC 420  
Db 361 CAAGTCCAGGATTGATCGTGGCCCTTACCTTGAGACACGCTCTGCTGACTGGATCCACAGC 420  
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Db 421 AGTGGCGGCTGGCGGCACTTCAACAGCTCTATACGGGACGGGGCGCTTGAGAGACGACGG 480  
QY 481 CGTCTGCGGAGGGCAACTGGGCATGATGAGACACAGTGTGACGGGGCGCTGGCACTG 540  
Db 481 CGTCTGCGGAGGGCAACTGGGCATGATGAGAGACAGTGTGACGGGGCGCTGGCACTG 540  
QY 541 GGGGCCCTGGTAACTGTAGGGGCGCTTTTGTCTAGCAAG 579  
Db 541 GGGGCCCTGGTAACTGTAGGGGCGCTTTTGTCTAGCAAG 579

RESULT 12  
LOCUS AX481423 582 bp DNA linear PAT 16-AUG-2002  
DEFINITION Sequence 37 from Patent WO02055693.  
ACCESSION AX481423  
VERSION AX481423.1 GI:22316337  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Kreutzer,R., Limmer,S., Rost,S. and Hadwiger,P.  
TITLE Method for inhibiting the expression of a target gene  
JOURNAL Patent: WO 02055693-A 37 18-JUL-2002;  
Ribopharma AG (DE)  
FEATURES location/Qualifiers  
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ORIGIN

Query Match 87.1%; Score 505.8; DB 6; Length 582;  
Best Local Similarity 91.9%; Pred. No. 4.3e-108;  
Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGGCTTCAACCCCAAGACACACGCGCTTGTGGCTGACTTTGTAGGCTAT 60  
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QY 61 AGGCTGAGGCAAGAGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGCCGCGGAC 120  
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QY 121 CCGCTGACCAAGCCATGCGGGCTGCTGAGAGACGAGTTTGAGACCCGTTCCGCGGAC 180  
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OY		361	CAAGTCCAGATTGATCGTGCCCTACCTGGAGACACGTCTGCCTGACTGATCCACAGC	420
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OY		421	AGTGGCGGCTGGCGGACTTGA	480
Db		421	AGTGGGGGCTGGCGGAGTTCA	480
OY		481	CGTCTGCCGGAGGGCACTGGGCATGAGT	540
Db		481	CGTCTCGCGGAGGGGAACTGGGCATGAGT	540
OY		541	GGGGCCCTGCTA	581
Db		541	GGGGCCCTGCTA	581
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LOCUS	HSU59747	582 bp	mRNA	linear PRI 29-SEP-1996
DEFINITION	Human Bcl-w (bcl-w) mRNA, complete cds.			
ACCESSION	U59747			
VERSION	U59747.1	GI:1572492		
KEYWORDS	.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 582)			
TITLE	Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G., Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.			
JOURNAL	bcl-w, a novel member of the bcl-2 family, promotes cell survival			
MEDLINE	Oncogene 13 (4), 665-675 (1996)			
PUBMED	96358615			
REFERENCE	8761287			
AUTHORS	2 (bases 1 to 582)			
TITLE	Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and Cory,S.			
JOURNAL	Direct Submission			
FEATURES	Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia			
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	RREGNMASVRIVLTGAVALGALTVAFPASK"			
ORIGIN				
Query Match	87.1%; Score 505.8; DB 9; Length 582;			
Best Local Similarity	91.9%; Pred. No. 4.3e-108;			
Matches 534; Conservative	0; Mismatches 47; Indels 0; Gaps 0;			
OY		1	ATGCCGACCCCCAGCCTCAACCCCAACAACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT	60
Db		1	ATGCCGACCCCCAGCCTCGGCCCCAGACACACGCGCTCTGTGGCAGACTTTGTAGGTTAT	60
OY		61	AGCGTGAGGCAGAAAGGTTATGTCTGTGGAGCTGGGCTGGGGAGAAGCCCAGCCGCCGAC	120

Db 61 AAGCTGAGGCAGAAAGGGTTATGTTCTGTGAGCTGGCCCCGGGGAGAGGCCACGACGTGAC 120

QY 121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGATTTAGACCCGTTTCCGCCGACC 180

Db 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTGAGACCCTTCCGGCGCACC 180

QY 181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCGAGGCTCAGCCAGCAACGCTTCACC 240

Db 181 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240

QY 241 CAGGTTCCGACGAACCTTTCCAAAGGGGGCCCTAACTGGGCGCTTGTGCAATCTTT 300

Db 241 CAGGCTCCGACGAACCTTTTCAAGGGGGCCCAACTGGGCGCCTTGTAGCCTTCTT 300

QY 301 GTCTTTGGGGCTGCCCTGTCGTCGTAGAGTGTCAACAAGAAATGAGCCCTTTGGTGGGA 360

Db 301 GTCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA 360

QY 361 CAAGTCCAGGATTGGATCGTGCCCTACCTGGAGACACGTCGTGGCTGACTGGATCCACAGC 420

Db 361 CAAGTCAGAGATGATGTGGCCTTACCTGGAGACGCGCTGGCTGACTGATCCACAGC 420

QY 421 AGTGGCGGCTGGCGGACTTCAAGCTCTATACGGGGACGGGCGCTTGAGAGACGCACGG 480

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QY 481 CGTCTCGGGAGGGCACTGGGCATGAGTGAGCACAGTGTGACGGGGCGGTGCACTG 540

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Db 541 GGGGCGCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581

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RESULT 14
D87461 LOCUS 3542 bp mRNA linear PRI 10-JAN-2004
DEFINITION Homo sapiens mRNA for KIAA0271 gene, partial cds.
ACCESSION D87461
VERSION D87461.1 GI:1944417
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayashi,Y.,
Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N.
TITLE Prediction of the coding sequences of unidentified human genes. VI.
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
analysis of cDNA clones from cell line KG-1 and brain
JOURNAL DNA Res. 3 (5), 321-329 (1996)
MEDLINE 97191544
PUBMED 9039502
REFERENCE
2 (bases 1 to 3542)
AUTHORS Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute;
1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
FEATURES
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GDGALAEARRRLREGNMWASVRTVLTGAVALGALVTVGAEFFASK"

ORIGIN

Query Match	86.5%;	Score 502.6;	DB 9;	Length 3542;
Best Local Similarity	91.6%;	Pred. No. 1.8e-107;		
Matches 532;	Conservative 0;	Mismatches 49;	Indels 0;	Gaps 0
QY 1	ATGCCGACCCACGCTCAACCCCAAGACACACGCGCTCTAGTGCGTGACTTTGTAGGCTAT	60		
Db 177	ATGGCGACCCACGCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT	236		
QY 61	AGCGTAGGCAGAAAGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGCCCGAC	120		
Db 237	AAGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGCCCCGGGAGGGCCAGACAGCTGAC	296		
QY 121	CCGCTGCACCAAGCCATGCGGCTGCTGAGACGAGTTTGAGACCCTTTCCGCCGACC	180		
Db 297	CCGCTGCACCAAGCCATGCGGCACTGAGATGAGTTCGAGACCCGCTTCCGCCGACC	356		
QY 181	TTCTCTGACCTGGCCGCTCAGCTACGTGACCCAGGCTCAGCCCAAGCAGCTTCACC	240		
Db 357	TTCTCTGATCTGGCGCTCAGCTGCACTGTGACCCAGGCTCAGCCCAACAGCTTCACC	416		
QY 241	CAGGTTCCGACGAACCTTTTCCAAGGGGGCCCTAACTGGGCCGCTCTTGTGCACTCTTT	300		
Db 417	CAGGCTCCGATGAACCTTTTCCAAGGGGGCCCAACTGGGCCGCTTGTAGCCTTCTTT	476		
QY 301	GTCTTTGGGGCTGCCCTGTGTGTGAGAGTGTCAACAAGAATGAGCCTTTGGTGGGA	360		
Db 477	GTCTTTGGGGCTGCACCTGTGTGTGAGAGTGTCAACAAGAGATGGAACCACTGCTGGGA	536		
QY 361	CAAGTCCAGGATTGATCGTGGCCTACCTGGAGACACGCTCTGGCTGACTGATCCACAGC	420		
Db 537	CAAGTCAGGAGTGGATGCTGGCCTACCTGGAGACCGCGCTGGCTGACTGATCCACAGC	596		
QY 421	AGTGGCGGCTGGGCGGACTTCAACAGCTCTAATACGGGGACGGGGCCCTGGAGGACGCA	480		
Db 597	AGTGGGGGCTGGGCGGAGTTCAACAGCTCTAATACGGGGACGGGGCCCTGGAGGAGGCGCGG	656		
QY 481	CGTCTGCGGAGGGGCAACTGGGCATGAGTGAACACAGTGTGACGGGGGSCGTGGCACTG	540		
Db 657	CGTCTGCGGAGGGGCAACTGGGCATCAGTGAAGACAGTGTGACGGGGGSCGTGGCACTG	716		
QY 541	GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAGTG 581			
Db 717	GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAGTG 757			

RESULT 15  
CO730429

CQ730429

## LOCUS

**DEFINITION** Sequence 16363 from Patent WO02068579.

**ACCESSIO**

VERSION

## KEYWORDS

**SOURCE**

## ORGANI

**DISCUSSION**

## REFERENCES

**AUTHORS** Venter, C.O., Adams, M.C., Li, P.W. and Myers, E.W.

TITLE	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL	Patent: WO 02068579-A 16363 06-SEP-2002; PE Corporation (NY) (US)
FEATURES	location/Qualifiers
source	1. .582

## ORIGIN

Query Match	Best Local Similarity	86.2%;	Score 501;	DB 6;	Length 582;
Matches	531;	Conservative	0;	Mismatches	50;
				Indels	0;
				Gaps	0
QY	1	ATGCCGACCCCGACCCCTCAACCCCGACACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT	60		
Db	1	ATGGCGACCCCGACCCCTCGGCCCGACACACACGCGCTCTGTGGCAGACTTTGTAGGTTAT	60		
QY	61	AGCGTGAGGCAGAGGGTTATGTCTGTGAGCTGGGCTGGGGAGGCCAGCCCGGAC	120		
Db	61	AACTGAGGCAGAGGGTTATGTCTGTGAGCTGGCCCGGGAGGGCCAGACAGCTGAC	120		
QY	121	CCGCTGCACCAAGCCATGCGGCTGCTGGAGACGAGTTGACCCCGTTTCCGCCGAC	180		
Db	121	CCACTGCACCAAGCCATGCGGCGAGCTGGAGATGAGTTGAGACCCGCTTCCGCCGAC	180		
QY	181	TTCTCTGACCTGGCCGCTAGCTACACGTGACCCAGGCTCAGCCAGCAACGCTTACC	240		
Db	181	TTCTCTGATCTGGCGCTCAGCTGATGTGACCCAGGCTCAGCCCAACAGCTTACC	240		
QY	241	CAGGTTCCGACGAATTTTCCAAGGGGGCCCTAACTGGGCGCTTGTGGCATTTCTT	300		
Db	241	CAGGTTCCGATGAATTTTCCAAGGGGGCCCACTGGGCGCTTGTAGCTTTCTT	300		
QY	301	GTCTTTGGGCTGCCCTGCTGTGCTGAGAGTGTCAACAAGAAATGAGCCTTTGGTGGGA	360		
Db	301	GTCTTTGGGCTGCACCTGTGTGTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA	360		
QY	361	CAAGTCCAGGATTTGATCGTGCCCTAAGTGGAGACACGTCTGCTGACTGATCCACAGC	420		
Db	361	CAAGTCCAGGATTTGATGTGTGCTTAACTGGAGACGCGGCTGCTGACTGATCCACAGC	420		
QY	421	AGTGCGGCTGGGCGGACTTCAAGCTCTATACGGGGACGGGCGCTTGGAGGACGCA	480		
Db	421	AGTGCGGCTGGGCGGAGTTCAAGCTCTATACGGGGACGGGCGCTTGGAGGAGCGCGG	480		
QY	481	CGTCTGCGGAGGGGCACTGGGCATGAGTGAGCAAGTGTGACGGGGCGCTGGCACTG	540		
Db	481	CGTCTGCGGAGGGGCACTGGGCATGAGTGAGCAAGTGTGACGGGGCGCTGGCACTG	540		
QY	541	GGGGCCCTGGTACTGTAGGGGCTTTTGTCTAGCAAGTG	581		
Db	541	GGGGCCCTGGTACTGTAGGGGCTTTTGTCTAGCAAGTG	581		

Search completed: April 10, 2005, 18:37:59  
Job time : 3063.74 secs

Job time : 3063.74 secs







QY 421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGAACGGGGCCCTGTGAGAGACGCAACGG 480  
DB 421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGAACGGGGCCCTGTGAGAGACGCAACGG 480  
QY 481 CGTCTGCGGAGGGCACTGGGCATGAGTGACAGCTGTGACGGGGCCGTGGCACTG 540  
DB 481 CGTCTGCGGAGGGCACTGGGCATGAGTGACAGCTGTGACGGGGCCGTGGCACTG 540  
QY 541 GGGGCCCTGTACTGTAGGGCCCTTTTGTAGCAAGTG 581  
DB 541 GGGGCCCTGTACTGTAGGGCCCTTTTGTAGCAAGTG 581

RESULT 3  
AAK25133  
ID AAK25133 standard; DNA; 581 BP.

XX AAK25133;

DT 05-JUL-1999 (first entry)

DE Mouse bcl-w gene.

KW Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;

KW animal model; ss.

OS Mus sp.

PN W09913710-A1.

XX 25-MAR-1999.

PF 16-SEP-1998; 98WO-AU000764.

PR 16-SEP-1997; 97AU-00009228.

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

PI Cory S, Adams J, Print C, Gibson L, Koentgen F;

DR WPI; 1999-243890/20.

DR P-PSDB; AAY05531.

PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
protein associated with Bcl-w.

PS Claim 3; Page 34; 52pp; English.

CC The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see  
CC AAY05531), a pro-survival member of the Bcl-2 family which is widely  
CC expressed and which is essential for spermatogenesis. The invention  
CC relates generally to a method of treatment and to an animal model for the  
CC identification of molecules and genetic sequences useful for inducing or  
CC reducing fertility of male animals. Methods are provided for the  
CC treatment of infertility, or for reducing fertility, by modulating  
CC spermatogenesis. An animal model carries a mutation is at least one  
CC allele of the human or murine bcl-w gene or in a gene associated with bcl  
CC -w. Such animals have disorganised seminiferous tubules and are  
CC substantially infertile, but possess no other major abnormalities as  
CC determined by histological examination. They can be used to screen for  
CC therapeutic molecules including genetic sequences capable of inducing,  
CC enhancing or otherwise facilitating spermatogenesis in animals, or which  
CC can induce infertility

SO Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 U; 0 Other;

Query Match 96.4%; Score 560.2; DB 2; Length 581;  
Best Local Similarity 97.8%; Pred. No. 3.8e-142;  
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGCTCAACCCAGACACACGGCTCTAGTGCTACTTTGAGGCTAT 60  
|||||

DB 1 ATGCCGACCCCAAGCTCAACCCAGACACACGGGCTCTAGTGCTACTTTGAGGCTAT 60  
QY 61 AGGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGGCTGGGGAAGCCAGCCGGAC 120  
DB 61 AAGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGGCTGGGGAAGCCAGCCGGAC 120  
QY 121 CCGCTGACCAAGCCATGCGGGCTGTGAGACGAGTTTGAGACCCGTTCCGGCCAC 180  
DB 121 CCGCTGACCAAGCCATGCGGGCTGTGAGACGAGTTTGAGACCCGTTCCGGCCAC 180  
QY 181 TTCTTGACCTGGCCGCTCAGCTTACAGTGACCCCAAGGCTCAGCCAGCAACGCTTACC 240  
DB 181 TTCTTGACCTGGCCGCTCAGCTTACAGTGACCCCAAGGCTCAGCCAGCAACGCTTACC 240  
QY 241 CAGGTTTCGACGAACCTTTCCAAAGGGGCCCTAAGCTGGGGCCGTCTGTGCAATCTTT 300  
DB 241 CAGGTTTCGACGAACCTTTCCAAAGGGGCCCTAAGCTGGGGCCGTCTGTGCAATCTTT 300  
QY 301 GTCTTTGGGCTGCCCCCTGTGTGTGCTGAGAGTGTCACAAAGAAATGAGCCCTTGTGGGA 360  
DB 301 GTCTTTGGGCTGCCCCCTGTGTGTGCTGAGAGTGTCACAAAGAAATGAGCCCTTGTGGGA 360  
QY 361 CAAGTCCAGATTGATCGTGCCCTAAGTGAAGACACAGTCTGGCTGATCCACAGC 420  
DB 361 CAAGTCCAGATTGATCGTGCCCTAAGTGAAGACACAGTCTGGCTGATCCACAGC 420  
QY 421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGAACGGGGCCCTGAGAGACGACGG 480  
DB 421 AGTGGCGGCTGGGCGGAGTTTCAAGCTCTATACGGGGAACGGGGCCCTGAGAGACGACGG 480  
QY 481 CGTCTGCGGAGGGCAACTGGGCATGATGAGCACAGTGCTGACGGGGCCGTGGCACTG 540  
DB 481 CGTCTGCGGAGGGCAACTGGGCATGATGAGCACAGTGCTGACGGGGCCGTGGCACTG 540  
QY 541 GGGGCCCTGTACTGTAGGGCCCTTTTGTAGCAAGTG 581  
DB 541 GGGGCCCTGTACTGTAGGGCCCTTTTGTAGCAAGTG 581

RESULT 4

ADB52996  
ID ADB52996 standard; DNA; 582 BP.

XX ADB52996;

DT 04-DEC-2003 (first entry)

DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3538.

KW toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;  
KW toxicity marker; toxicity progression; drug screening;  
KW primary rat hepatocyte toxicity modelling; gene; ds.

OS Rattus norvegicus.

PN W02003065993-A2.

XX 14-AUG-2003.

PF 04-FEB-2003; 2003WO-US003482.

XX 04-FEB-2002; 2002US-0353171P.

PR 13-MAR-2002; 2002US-0363534P.

PR 08-APR-2002; 2002US-0370248P.

PR 10-APR-2002; 2002US-0371134P.

PR 10-APR-2002; 2002US-0371135P.

PR 11-APR-2002; 2002US-0371413P.

PR 19-APR-2002; 2002US-0373601P.

PR 19-APR-2002; 2002US-0373602P.

PR 22-APR-2002; 2002US-0374139P.

PR 08-MAY-2002; 2002US-0378370P.

PR 09-MAY-2002; 2002US-0378652P.

PR 09-MAY-2002; 2002US-0378653P.  
PR 09-MAY-2002; 2002US-0378665P.  
PR 09-JUL-2002; 2002US-0394230P.  
PR 09-JUL-2002; 2002US-0394253P.  
PR 04-SEP-2002; 2002US-0407688P.  
PR 28-JAN-2003; 2003US-0442900P.  
XX  
XX (GENE-) GENE LOGIC INC.

PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;  
PI Elashoff M;  
XX  
XX WPI; 2003-731472/69.

PT Determining if a compound induces a toxic effect on a tissue or cell, for  
PT identifying hepatotoxic compounds, comprises comparing a gene expression  
PT profile of a tissue or cell sample to a database of Tox mean and non-Tox  
XX mean values.

PS Claim 44; SEQ ID NO 3538; 874pp; English.

XX  
XX  
XX The present invention describes a method for determining whether a  
XX compound induces a toxic effect on a tissue or cell. The method comprises  
XX preparing a gene expression profile of a tissue or cell sample exposed to  
XX the compound, and comparing the gene expression profile to a database  
XX comprising data or information on the Tox mean and non-Tox mean value.  
XX The method is useful for predicting or identifying at least one toxic  
XX effect, particularly hepatotoxicity, of a test or unknown compound. The  
XX genes listed in the specification are useful as diagnostic or toxicity  
XX markers for the prediction or identification of the physiological state  
XX of tissue or cell sample that has been exposed to a compound, or to  
XX identify or predict the toxic effects of a compound or an agent. These  
XX may also be used as markers for monitoring toxicity progression or for  
XX drug screening. The present sequence represents a primary rat hepatocyte  
XX toxicity modelling related gene sequence from the present invention.  
SQ Sequence 582 BP; 111 A; 157 C; 200 G; 114 T; 0 U; 0 Other;

Query Match 93.7%; Score 544.2; DB 10; Length 582;  
Best Local Similarity 96.0%; Pred. No. 8.5e-138;  
Matches 558; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 ATGCCGACCCAGCCTCAACCCAGACACACGCGCTAGTGGCTGACTTTGAGGCTAT 60  
Db 1 ATGCCGACCCAGCCTCAACCCAGACACACGCGCTAGTGGCTGACTTTGAGGCTAT 60  
QY 61 AGGCTGAGGACAGAGGTTATGTCGAGAGCTGGGCTGGGAGGCCAGCCGCCGAC 120  
Db 61 AGGCTGAGGACAGAGGTTATGTCGAGAGCTGGGCTGGGAGGCCAGCCGCCGAC 120  
QY 121 CCGCTGCACCAAGCCATGCGGCTGTGAGAGCAGATTGAGACCCGCTTCCGCCGAC 180  
Db 121 CCGCTGCACCAAGCCATGCGGCTGTGAGAGCAGATTGAGACCCGCTTCCGCCGAC 180  
QY 181 TTCTGTACCTGGCCGCTCAGCTACAGTGAACCCAGGCTCAGCCAGCAACGCTTAC 240  
Db 181 TTCTGTACCTGGCCGCTCAGCTACAGTGAACCCAGGCTCAGCCAGCAACGCTTAC 240  
QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGCCCCCTAAGTGGGCGCTTGTGCAATTCTT 300  
Db 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGCCCCCTAAGTGGGCGCTTGTGCAATTCTT 300  
QY 301 GTCTTTGGGGTCCCTGTGTGTGAGAGTGTCAACAAGAATGAGGCTTGTGGGA 360  
Db 301 GTCTTTGGGGTCCCTGTGTGTGAGAGTGTCAACAAGAATGAGGCTTGTGGGA 360  
QY 361 CAAGTCCAGGATGATCGTGGCTTACCTGAGACACGCTGTGCTGACTGATCCACAGC 420  
Db 361 CAAGTCCAGGATGATCGTGGCTTACCTGAGACACGCTGTGCTGACTGATCCACAGC 420  
QY 421 AGTGGCGGCTGGCGGACTTCAACAGCTCTATACGGGGACGGGGCCCTGGAGGACGACGG 480  
Db 421 AGTGGCGGCTGGCGGACTTCAACAGCTCTATACGGGGACGGGGCCCTGGAGGACGACGG 480

QY 481 CGTCTGCGGAGGCACTGGGCAATGAGTACAGACAGTGTGACGGGGCCGTGGCACTG 540  
Db 481 CGTCTGCGGAGGCACTGGGCAATGAGTACAGACAGTGTGACGGGGCCGTGGCACTG 540  
QY 541 GGGGCGCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581  
Db 541 GGGGCGCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581

RESULT 5  
AAV28333  
ID AAV28333 standard; cDNA; 579 BP.  
XX  
XX  
XX AAV28333;  
AC  
XX  
DT 02-OCT-1998 (first entry)  
XX  
DE Rat bcl-Y gene.  
XX  
KW ss; bcl-Y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.  
XX  
OS Rattus sp.

XX  
XX Key Location/Qualifiers  
FT CDS 1..579  
FT /\*tag= a  
FT /product= "bcl-y"  
FT /note= "No stop codon given"

PN US5789201-A.  
XX  
PD 04-AUG-1998.  
XX  
PF 11-FEB-1997; 97US-00798897.  
XX  
PR 23-FEB-1996; 96US-0012201P.  
XX  
PA (COCE-) COCENSYS INC.

PI Guastella J;  
XX  
DR WPI; 1998-446079/38.  
DR P-PSDB; AAM61391.

PT Nucleic acids encoding B-cell lymphoma-Y protein - useful for producing  
PT recombinant protein for use in treating uncontrolled cell growth e.g.  
XX cancers.

PS Claim 2; Column 13/14; 27pp; English.

XX  
XX The mammalian bcl-Y genes encode a protein that is a member of the bcl-2  
XX family, components in the cell death pathway. The bcl-2 family have both  
XX apoptotic activity and the apoptosis blocking activity. bcl-Y falls in  
XX the apoptosis activity category. The recombinant protein may be used to  
XX prevent uncontrolled cell growth, either by its direct administration to  
XX recombinant genetic constructs to increase its expression in vivo. Also,  
XX death is desired  
XX

SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;  
Query Match 93.0%; Score 540.6; DB 2; Length 579;  
Best Local Similarity 95.9%; Pred. No. 8e-137;  
Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 ATGCCGACCCAGCCTCAACCCAGACACACGCGCTAGTGGCTGACTTTGAGGCTAT 60  
Db 1 ATGCCGACCCAGCCTCAACCCAGACACACGCGCTAGTGGCTGACTTTGAGGCTAT 60  
QY 61 AGCTGAGACAGAGGTTATGTCGTGAGAGCTGGGCTGGGGAAGGCCAGCCGCCGAC 120  
Db 61 AGCTGAGACAGAGGTTATGTCGTGAGAGCTGGGCTGGGGAAGGCCAGCCGCCGAC 120



QY 121 CCGCTGCACCAAGCCATGCGGGCTGCTGAGACGAGTTTGAGACCCCGTTCCCGCCGACC 180  
DB 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCCGCTTCCGCGCACC 180  
QY 181 TTCTCTGACCTGGCGCTCAGCTACACGTGAGCCCGAGCTCAGCCCGACGAGCTTACC 240  
DB 181 TTCTCTGACCTGGCGCTCAGCTACACGTGAGCCCGAGCTCAGCCCGACGAGCTTACC 240  
QY 241 CAGGTTTCCGACGAACTTTTCCAGGGGGCCCTAATGCGGCGCTTGTGCAATTTCTT 300  
DB 241 CAGGTTTCCGACGAACTTTTCCAGGGGGCCCGCACTGGGGCGCTTGTGCAATTTCTT 300  
QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAATGAGCCCTTGTGGGA 360  
DB 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAATGAGCCCAATTGGTGGGA 360  
QY 361 CAAGTCCAGGATTGGATCGTGGCTACCTGAGACACGCTGTGGCTGACTGGATCCACAGC 420  
DB 361 CAAGTCCAGGATTGGATCGTGGCTACCTGAGACACGCTTGGCTGACTGGATCCACAGC 420  
QY 421 AGTGGCGGCTGGCGGACTTACAGCTCTATACGGGGACGGGGCCCTGAGAGACGACGG 480  
DB 421 AGTGGCGGCTGGCGGAGTTACAGCTCTATACGGGGACGGGGCCCTGAGAGACGACGG 480  
QY 481 CGTCTGCGGAGGCACTGGGCAATGAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540  
DB 481 CGTCTGCGGAGGGGAAGTGGGCATCAGTGAAGACAGTGTGACGGGGCGTGTGGCACTG 540  
QY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGTAACAAG 579  
DB 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGTAACAAG 579

RESULT 6  
AAK15945  
ID AAK15945 standard; cDNA; 579 BP.

AC AAK15945;  
XX 20-MAY-1999 (first entry)  
DE cDNA encoding the rat bcl-y protein.  
XX  
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
KW premature cell death; cell death stimulator; prolonged cell life span;  
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite;  
KW 88.  
XX  
OS Rattus sp.  
PN US5883229-A.  
XX 16-MAR-1999.  
PD 16-MAR-1999.  
XX 25-NOV-1997; 97US-00978523.  
PF 25-NOV-1997; 97US-00978523.  
XX 23-FEB-1996; 96US-0012201P.  
PR 11-FEB-1997; 97US-00798897.  
XX  
PA (COCE-) COCENSYS INC.  
XX  
PI Guastella J;  
XX  
DR WPI; 1999-214150/18.  
DR P-PSDB; AAW97391.  
XX  
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for  
modulating programmed cell death.

XX  
PS Disclosure; Col 13-16; 26pp; English.  
XX  
CC The present sequence encodes rat bcl-y protein (Rbcl-y). The  
CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and  
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in  
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y  
CC proteins may be used to treat conditions associated with a disruption of  
CC the cell death pathway. If they act as cell death inhibitors, they may be  
CC used in therapies to treat subjects suffering from: strokes, head trauma,  
CC Alzheimer's Disease, neural and muscular degenerative diseases  
CC (especially multiple sclerosis), myocardial infarction, vitally induced  
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis  
CC - conditions where cells under go premature cell death as a result of  
CC triggers which may or may not be apparent. They may also be used in this  
CC way to develop cell lines which remain viable in culture for an extended  
CC period. In contrast, if they act as cell death stimulators, Rbcl-y and  
CC Hbcl-y may be used to treat conditions associated with prolonged cell  
CC life span such as cancer (especially Kaposi's sarcoma and lung cancer)  
CC and auto/hyperimmune diseases. They may also be used to cause cell death  
CC in, and hence control, parasites  
XX  
SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;

Query Match 93.0%; Score 540.6; DB 2; Length 579;  
Best Local Similarity 95.9%; Pred. No. 8e-137;  
Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGCTTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
DB 1 ATGCCGACCCCAAGCTTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
QY 61 AGGCTGAGGAGAAAGGTTATGTCTGTGAGAGCTGGGCTGGGGAAGGCCAGCCCGGAC 120  
DB 61 AGGCTGAGGAGAAAGGTTATGTCTGTGAGAGCTGGGCTGGGGAAGGCCAGCCCGGAC 120  
QY 121 CCGCTGCACCAAGCCATGCGGCTGCTGAGAGAGAGTTTGAGACCCGTTCCGCGCACC 180  
DB 121 CCGCTGCACCAAGCCATGCGGCTGCTGAGAGAGAGTTTGAGACCCGTTCCGCGCACC 180  
QY 181 TTCTCTGACCTGGCGGCTCAGCTACACGTGAGCCCGAGCTCAGCCCGACGCTTACC 240  
DB 181 TTCTCTGACCTGGCGGCTCAGCTACACGTGAGCCCGAGCTCAGCCCGACGCTTACC 240  
QY 241 CAGGTTTCCGACGAACTTTTCCAGGGGGCCCTAATGCGGCGCTTGTGCAATTTCTT 300  
DB 241 CAGGTTTCCGACGAACTTTTCCAGGGGGCCCGCACTGGGGCGCTTGTGCAATTTCTT 300  
QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAATGAGCCCTTGTGGGA 360  
DB 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAATGAGCCCTTGTGGGA 360  
QY 361 CAAGTCCAGGATTGGATCGTGGCTACCTGAGACACGCTGTGGCTGACTGGATCCACAGC 420  
DB 361 CAAGTCCAGGATTGGATCGTGGCTACCTGAGACACGCTGTGGCTGACTGGATCCACAGC 420  
QY 421 AGTGGCGGCTGGCGGACTTACAGCTCTATACGGGGACGGGGCCCTGAGAGACGACGG 480  
DB 421 AGTGGCGGCTGGCGGAGTTACAGCTCTATACGGGGACGGGGCCCTGAGAGACGACGG 480  
QY 481 CGTCTGCGGAGGCACTGGGCAATGAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540  
DB 481 CGTCTGCGGAGGGGAAGTGGGCATCAGTGAAGACAGTGTGACGGGGCGTGTGGCACTG 540  
QY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGTAACAAG 579  
DB 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGTAACAAG 579

RESULT 7  
ABV78153  
ID ABV78153 standard; DNA; 582 BP.  
XX

AC ABV78153;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Human bcl-w DNA SEQ ID NO 37.  
XX  
KM RNA inhibition; dsRNAI; gene expression inhibitor; oncogene; cytostatic;  
XX virucide; protozoacide; gene; ds.  
OS Homo sapiens.  
XX  
PN WO200255693-A2.  
XX  
PD 18-JUL-2002.  
XX  
PF 09-JAN-2002; 2002WO-EP000152.  
XX  
PR 09-JAN-2001; 2001DE-01000586.  
PR 26-OCT-2001; 2001DE-01000586.  
PR 29-NOV-2001; 2001DE-01055280.  
PR 07-DEC-2001; 2001DE-01058411.  
XX  
PA (RIBO-) RIBOPHARMA AG.  
XX  
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;  
XX  
DR WPI; 2002-590671/63.  
XX  
PT Inhibiting expression of target gene, useful e.g. for inhibiting  
PT oncogenes, by administering double-stranded RNA complementary to the  
XX target and having an overhang.  
PS Claim 10; Page 134; 203pp; German.  
XX  
CC The invention relates to inhibiting expression of a target gene (I) in a  
CC cell by introducing an inhibitory RNA (dsRNAI) having a double-stranded  
CC structure of at most 49 consecutive bases. At least part of one strand  
CC (as1) of dsRNAI is complementary to (I) and at least one end of dsRNAI  
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the  
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.  
CC in humans, also genes in plasmidium or in viruses or viroids that are  
CC pathogenic for humans, animals or plants. Introducing an overhang into  
CC dsRNA greatly increases effectiveness for inhibiting gene expression,  
CC both in vivo and in vitro and also increases stability and thus the  
CC effective concentration inside the cell. The present sequence is that of  
CC a gene related to the invention  
XX  
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match 87.1%; Score 505.8; DB 6; Length 582;  
Best Local Similarity 91.9%; Pred. No. 2.3e-127;  
Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCGCTCAACCCGAGACACACGCGCTCTAGTGGCTGACTTGTAGGCTAT 60  
DB 1 ATGGCGACCCCGCTCGGCCCCAGACACACGCGCTCTAGTGGCTGACTTGTAGGCTAT 60  
QY 61 AGGCTGAGGAGAGGGTTATGTCTGTGAGCTGGCGCTGGGAGAGGCCCGCCGAC 120  
DB 61 AAGCTGAGGAGAGGGTTATGTCTGTGAGCTGGCGCTGGGAGAGGCCCGCCGAC 120  
QY 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGCAGTTTGAAGCCGTTTCCGCGGAC 180  
DB 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGCAGTTTGAAGCCGTTTCCGCGGAC 180  
QY 181 TTCTCTGACTGGCGCTCAGCTACAGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
DB 181 TTCTCTGACTGGCGCTCAGCTACAGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
QY 241 CAGGTTTCCGAGCACTTTTCCAGAGGGGCTTAAGTGGCGCTTGTGGCATTCTTT 300  
DB 241 CAGGTTTCCGAGCACTTTTCCAGAGGGGCTTAAGTGGCGCTTGTGGCATTCTTT 300  
241 CAGGTTTCCGAGCACTTTTCCAGAGGGGCTTAAGTGGCGCTTGTGGCATTCTTT 300

QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGAGCCTTGTGGGA 360  
DB 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGAGCCTTGTGGGA 360  
QY 361 CAAATCCAGATTTGATCGTGGCTTACCTGAGACAGCTGTGGCTGATCCAGAC 420  
DB 361 CAAATCCAGATTTGATCGTGGCTTACCTGAGACAGCTGTGGCTGATCCAGAC 420  
QY 421 AGTGGCGGCTGGCGGAGCTTCAAGCTTATACGGGAGCGGGCCCTGAGAGCGCAG 480  
DB 421 AGTGGCGGCTGGCGGAGCTTCAAGCTTATACGGGAGCGGGCCCTGAGAGCGCAG 480  
QY 481 CGTCTGGGAGAGGCACTGGGCAATGATGAGCAGACAGTGTGACGGGGCCCTGGCACTG 540  
DB 481 CGTCTGGGAGAGGCACTGGGCAATGATGAGCAGACAGTGTGACGGGGCCCTGGCACTG 540  
QY 541 GGGGCCCCGTGTAAGTGTAGGGGCTTTTGTGTAAGCAAGTG 581  
DB 541 GGGGCCCCGTGTAAGTGTAGGGGCTTTTGTGTAAGCAAGTG 581

RESULT 8  
AB235729  
ID AB235729 standard; DNA; 582 BP.  
XX  
AC AB235729;  
XX  
DT 07-FEB-2003 (first entry)  
XX  
DE Human bcl-w polynucleotide SEQ ID NO 37.  
XX  
KM Double stranded RNA; dsRNA; RNAI; RNA inhibition; cytostatic; virucide;  
KM protozoacide; gene expression; antisense; tumour; infection; plasmidium;  
KM virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;  
XX Hepatitis C virus; human papilloma virus; gene; ds.  
OS Homo sapiens.  
XX  
PN DE10100588-A1.  
XX  
PD 18-JUL-2002.  
XX  
PF 09-JAN-2001; 2001DE-01000588.  
XX  
PR 09-JAN-2001; 2001DE-01000588.  
XX  
PA (RIBO-) RIBOPHARMA AG.  
XX  
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;  
XX  
DR WPI; 2002-683450/74.  
XX

Inhibiting expression of target genes, useful e.g. for treating tumors,  
by introducing into cells two double-stranded RNAs that are complementary  
to the target.

Claim 13; Page 30-31; 100pp; German.

The invention relates to inhibiting expression of a target gene in a cell  
by introducing at least two oligonucleotides (dsRNAI and II), both  
with a double-stranded (ds) structure of at most 49 sequential nucleotide  
pairs. At least part of one strand (S1, S2) of the ds structures in each  
of dsRNAI and II are complementary to regions in the target gene. The  
method uses antisense inhibition of gene expression using double stranded  
RNA inhibition (RNAI). The method is particularly used to treat tumors  
or infections, especially by plasmidium or viruses/viroids (pathogenic  
of humans, animals or plants). The method provides more effective inhibition  
of expression than known methods using a single dsRNA, even at very low  
concentrations. When dsRNA has at least one unpaired nucleotide at the  
end, stability (and thus effective concentration in the cell) is improved  
and efficiency can be increased further by pretreating the cells with  
interferon. The present sequence is that of a target DNA of the invention

Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match 87.1%; Score 505.8; DB 6; Length 582;  
Best Local Similarity 91.9%; Pred. No. 2.3e-127;  
Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

```
QY 1 ATGCCGACCCCAAGCTCAACCCAGACACACCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
    |||
DB 1 ATGGCGACCCCAAGCTCGGCCCCAGACACACCGGCTCTGGTGCGAGACTTTGTAGGTTAT 60
QY 61 AGGCTGAGGAGAGGGTTATGTCTGTGTGAGCTGGGCTGGGGAAGGCCCGCCGAC 120
    |||
DB 61 AAGCTGAGGAGAGGGTTATGTCTGTGTGAGCTGGGCCCCGGGAGAGGCCCGACAGCTGAC 120
QY 121 CCGCTGACCAAGCCATGCGGGCTGTGAGACGAGTTGAGACCCGTTCCGCGCAC 180
    |||
DB 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGTTCCGCGCAC 180
QY 181 TTCTGTGACCTGGCCGCTCAGCTACAGCTGACGCTCAGGCTCAGCCAGCAAGCTTACC 240
    |||
DB 181 TTCTGTGATCTGGCGGCTCAGCTGATGATGACCCAGGCTCAGCCAGCAAGCTTACC 240
QY 241 CAGGTTCCGACGAATTTTCCAGGGGGCCCTAATGCGGGCCGCTTGTGGCATTTCTT 300
    |||
DB 241 CAGGTTCCGACGAATTTTCAAGGGGGCCCAACTGCGGGCCGCTTGTAGCTTCTTT 300
QY 301 GTCTTTGGGGCTGCCCTGTGTGTGTGAGAGTGTCAACAAAGAAATGAGGCTTTGTGGGA 360
    |||
DB 301 GTCTTTGGGGCTGCACTGTGTGTGTGAGAGTGTCAACAAAGAGATGAGCACTGTGGGA 360
QY 361 CAAGTCCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
    |||
DB 361 CAAGTCCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 AGTGGCGGCTGGCGGCACTTCAAGCTCTATACGAGGAGCGGGCCCTGAGAGAGAGAGAG 480
    |||
DB 421 AGTGGCGGCTGGCGGCACTTCAAGCTCTATACGAGGAGCGGGCCCTGAGAGAGAGAGAG 480
QY 481 CGTCTGCGGAGGAGCACTGGGCACTGATGAGACAGAGTGTGACGGGGCCGTGGCACTG 540
    |||
DB 481 CGTCTGCGGAGGAGCACTGGGCACTGATGAGAGAGAGTGTGACGGGGCCGTGGCACTG 540
QY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581
    |||
DB 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581
```

## RESULT 9

ABX09972

ID ABX09972 standard; DNA; 582 BP.

AC ABX09972;

DT 23-JAN-2003 (first entry)

DE Human bcl-w DNA fragment SEQ ID 37.

KW Oligoribonucleotide; interferon; oncogene; cytokine; id; developmental;

KM prion; inhibition; human; ds.

OS Homo sapiens.

PN DE10100587-C1.

PD 21-NOV-2002.

PF 09-JAN-2001; 2001DB-01000587.

PR 09-JAN-2001; 2001DB-01000587.

PA (RIBO-) RIBOPHARMA AG.

PI Kreutzner R, Limmer S, Rost S, Hadwiger P;

XX DR WPI; 2002-742209/81.

XX PT Inhibiting expression of target genes, e.g. oncogenes, in cells, by  
PT introduction of complementary double-stranded oligoribonucleotide, after  
PT treating the cell with interferon.

XX PS Disclosure; Page 35-36; 98pp; German.

XX CC This invention describes a novel method for inhibiting expression of a  
CC target gene by introducing into the cell that contains the target gene at  
CC least one oligoribonucleotide (dsRNA) that has a double-stranded (ds)  
CC structure of not more than 49 consecutive nucleotides (nt), where at  
CC least a segment of one strand of the ds structure is complementary with  
CC the target gene and the cells are treated with interferon before  
CC introduction of dsRNA. The method is used to inhibit expression of  
CC target genes, particularly oncogenes, cytokine genes, id (not defined)  
CC protein genes; developmental or prion genes, or genes expressed in  
CC pathogenic organisms (particularly plasmids) or in viruses or viroids  
CC (pathogenic in humans, animals or plants). Treating the cells with  
CC interferon greatly increases the extent to which dsRNA can inhibit  
CC expression of the target genes, and the effect is even greater when dsRNA  
CC are modified to increase their stability. ABX09936-ABX10075 represent  
CC gene fragments used to illustrate the method of the invention

XX SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match 87.1%; Score 505.8; DB 6; Length 582;  
Best Local Similarity 91.9%; Pred. No. 2.3e-127;  
Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

```
QY 1 ATGCCGACCCCAAGCTCAACCCAGACACACCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
    |||
DB 1 ATGGCGACCCCAAGCTCGGCCCCAGACACACCGGCTCTGGTGCGAGACTTTGTAGGTTAT 60
QY 61 AGGCTGAGGAGAGGGTTATGTCTGTGTGAGCTGGGCTGGGGAAGGCCCGCCGAC 120
    |||
DB 61 AAGCTGAGGAGAGGGTTATGTCTGTGTGAGCTGGGCCCCGGGAGAGGCCCGACAGCTGAC 120
QY 121 CCGCTGACCAAGCCATGCGGGCTGTGAGAGAGAGTTGAGACCCGTTCCGCGCAC 180
    |||
DB 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGTTCCGCGCAC 180
QY 181 TTCTGTGACCTGGCCGCTCAGCTACAGCTGACGCTCAGGCTCAGCCAGCAAGCTTACC 240
    |||
DB 181 TTCTGTGATCTGGCGGCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 CAGGTTCCGACGAATTTTCCAGGGGGCCCTAATGCGGGCCGCTTGTGGCATTTCTT 300
    |||
DB 241 CAGGTTCCGACGAATTTTCAAGGGGGCCCAACTGCGGGCCGCTTGTAGCTTCTTT 300
QY 301 GTCTTTGGGGCTGCCCTGTGTGTGTGAGAGTGTCAACAAAGAAATGAGGCTTTGTGGGA 360
    |||
DB 301 GTCTTTGGGGCTGCACTGTGTGTGTGAGAGTGTCAACAAAGAGATGAGCACTGTGGGA 360
QY 361 CAAGTCCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
    |||
DB 361 CAAGTCCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 AGTGGCGGCTGGCGGCACTTCAAGCTCTATACGAGGAGCGGGCCCTGAGAGAGAGAGAG 480
    |||
DB 421 AGTGGCGGCTGGCGGCACTTCAAGCTCTATACGAGGAGCGGGCCCTGAGAGAGAGAGAG 480
QY 481 CGTCTGCGGAGGAGCACTGGGCACTGATGAGACAGAGTGTGACGGGGCCGTGGCACTG 540
    |||
DB 481 CGTCTGCGGAGGAGCACTGGGCACTGATGAGAGAGAGTGTGACGGGGCCGTGGCACTG 540
QY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581
    |||
DB 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581
```

## RESULT 10



ABL91694  
ID ABL91694 standard; DNA; 582 BP.  
XX  
AC ABL91694;  
XX  
DT 28-MAY-2002 (first entry)  
XX  
DE Human polynucleotide SEQ ID NO 37.  
XX  
KW Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;  
KW plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;  
KW cytosolic; virucide; protozoacide; antibacterial; ds.  
OS  
XX Homo sapiens.  
XX  
PN DE10100586-C1.  
XX  
PD 11-APR-2002.  
XX  
PF 09-JAN-2001; 2001DE-0100586.  
XX  
PR 09-JAN-2001; 2001DE-0100586.  
XX  
PA (RIBO-) RIBOPHARMA AG.  
XX  
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;  
XX  
DR WPI; 2002-270454/32.  
XX  
PT Inhibiting gene expression in cells, useful for e.g. treating tumors, by  
PT introducing double-stranded complementary oligoRNA having unpaired  
PT terminal bases.  
XX  
PS Claim 13; Page 32; 104pp; German.  
XX  
CC The invention relates to a method for inhibiting expression of a target  
CC gene (ABL91658-ABL91797) in a cell by introducing at least one  
CC oligoribonucleotide that has a double-stranded structure consisting of at  
CC most 49 sequential nucleotide pairs, with at least part of one strand  
CC complementary with the target gene and has at least one end a single-  
CC stranded segment of 1-4 nt. The method provides oligoribonucleotides for  
CC antisense inhibition of gene expression useful e.g. for treating tumors  
CC but the oligoribonucleotides may also be directed against genes present  
CC in pathogens (e.g. Plasmodium or viruses/viroids), pathogenic on humans,  
CC animals or plants) or against cytokine, Id, developmental or prion genes.  
CC The method provides more effective inhibition of gene expression than use  
CC of known oligonucleotides, probably because the unpaired overhang  
CC increases stability and thus intracellular concentration  
XX  
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;  
Query Match 87.1%; Score 505.8; DB 6; Length 582;  
Best Local Similarity 91.9%; Pred. No. 2.3e-127;  
Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
QY 1 ATGCCGACCCCGACCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
Db 1 ATGGCGACCCCGACCTCGCCCGACACACGCGCTCTGTGGCAGACTTTGTAGGTTAT 60  
QY 61 AGCTGAGGACAGAGGCTTATGTCTGTGAGCTGGCGCTGGGGAAGGCCCGCCGCGAC 120  
Db 61 AAGCTGAGGACAGAGGCTTATGTCTGTGAGCTGGCGCCCGGAGGCGCCAGAGCTGAC 120  
QY 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGAGATTGAGACCCGTTTCCGCGCACC 180  
Db 121 CCGCTGACCAAGCCATGCGGCGAGCTGAGATGATTCGAGACCCGCTTCCGCGCACC 180  
QY 181 TTCTCTGACTGGCGCTCAGCTACAGTGACGCCAGGCTCAGCCAGCAAGCTTCAAC 240  
Db 181 TTCTCTGACTGGCGCTCAGCTACAGTGACGCCAGGCTCAGCCAGCAAGCTTCAAC 240  
QY 241 CAGGTTCCGACGACTTTTCCAGAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCTT 300  
Db 241 CAGGTTCCGACGACTTTTCCAGAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCTT 300

Db 241 CAGGTTCCGACGACTTTTTCAGAGGGGCGCCCAACTGGGGCGCCCTTGTAGCCTTCTTT 300  
QY 301 GTCTTTGGGCTGCCCTGTGTCTGAGAGTGTCAACAAGAATGAGCCTTTGTGGGA 360  
Db 301 GTCTTTGGGCTGCCACTGTGTCTGAGAGTGTCAACAAGAATGAGATGAACTGTGGGA 360  
QY 361 CAAGTCCAGATTGATCGTGCCCTACCTGAGACACAGTCTGGCTGACTGATCCACAGC 420  
Db 361 CAAGTCCAGATTGATGATGTGGCCCTACCTGAGACACAGTCTGGCTGACTGATCCACAGC 420  
QY 421 AGTGGCGCTGGCGGACTTCACAGCTTATACGGGACGGGCGCCCTGAGAGCGCACGG 480  
Db 421 AGTGGCGCTGGCGGAGTTACAGCTTATACGGGACGGGCGCCCTGAGAGCGCACGG 480  
QY 481 CGTCTGCGGAGGCACTGGGCATGATGACACAGTGTGTGACGGGCGGTGGCACTG 540  
Db 481 CGTCTGCGGAGGGAAGTGGGCATGATGAGACAGTGTGTGACGGGCGGTGGCACTG 540  
QY 541 GGGGCGCTGTAACTGTAGGGGCGCTTTTGTCTAGCAAGTG 581  
Db 541 GGGGCGCTGTAACTGTAGGGGCGCTTTTGTCTAGCAAGTG 581

RESULT 11  
AAX25132  
ID AAX25132 standard; DNA; 581 BP.  
XX  
AC AAX25132;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Human bcl-w gene.  
XX  
KW Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;  
KW animal model; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO913710-A1.  
XX  
PD 25-MAR-1999.  
XX  
PF 16-SEP-1998; 98WO-AU000764.  
XX  
PR 16-SEP-1997; 97AU-00009228.  
XX  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX  
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;  
XX  
DR WPI; 1999-243890/20.  
XX  
DR P-PSDB; AAY05530.  
XX  
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
PT protein associated with Bcl-w.  
XX  
PS Claim 3; Page 32; 52pp; English.  
XX  
CC The present sequence is the human bcl-w gene encoding Bcl-w protein (see  
CC AAY05530), a pro-survival member of the Bcl-2 family which is widely  
CC expressed and which is essential for spermatogenesis. The invention  
CC relates generally to a method of treatment and to an animal model for the  
CC identification of molecules and genetic sequences useful for inducing or  
CC reducing fertility of male animals. Methods are provided for inducing or  
CC treatment of infertility, or for reducing fertility, by modulating  
CC spermatogenesis. An animal model carries a mutation is at least one  
CC allele of the human or murine bcl-w gene or in a gene associated with bcl  
CC -w. Such animals have disorganised seminiferous tubules and are  
CC substantially infertile, but possess no other major abnormalities as  
CC determined by histological examination. They can be used to screen for  
CC therapeutic molecules including genetic sequences capable of inducing,  
CC enhancing or otherwise facilitating spermatogenesis in animals, or which  
CC can induce infertility



XX Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 U; 0 Other;  
SQ

Query Match 86.5%; Score 502.6; DB 2; Length 581;  
Best Local Similarity 91.6%; Pred. No. 1.7e-126;  
Matches 532; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGCTTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
DB 1 ATGGCGACCCCAAGCTTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
QY 61 AGGCTGAGGAGAGAGGTTATGTCTGTGAGAGCTGGGCTGGGGAAGGCCGAGCCGCGAC 120  
DB 61 AAGCTGAGGAGAGAGGTTATGTCTGTGAGAGCTGGGCTGGGGAAGGCCGAGCGACTGAC 120  
QY 121 CCGCTGACCAAGCCATGCGGGCTGTGAGAGCAAGTTTGAGACCCGTTCCGCGCACCC 180  
DB 121 CCGCTGACCAAGCCATGCGGGCAAGCTGAGATGAGTTGAGACCCGCTTCCGCGCACCC 180  
QY 181 TTCTTGACCTGAGCCGCTCAGCTACACGTCGACCCGAGGCTCAGCCGAGCAAGCTTACC 240  
DB 181 TTCTTGATCTGAGCGGCTCAGCTGATGATGACCCGAGGCTCAGCCGAGCAAGCTTACC 240  
QY 241 CAGGTTTCCGAGCACTTTTCCAAAGGGGGCCCTTAAGTGGGCGCTTGTGCAATCTTT 300  
DB 241 CAGGTTTCCGAGCACTTTTCAAGGGGGCCCAAGTGGGCGCTTGTAGCCTTCTTT 300  
QY 301 GTCTTTGGGGCTGCCCTGTGTGTGAGAGTTCACAAAGAAATGAGCCTTTGGTGGA 360  
DB 301 GTCTTTGGGGCTGCACTGTGTGTGAGAGTTCACAAAGAGATGAGCACTGGTGGA 360  
QY 361 CAAGTCCAGAGATTGATCGTGCCCTACCTGAGACACGCTGTGCTGATCCACAGC 420  
DB 361 CAAGTCCAGAGATGATGCTGCGCTACCTGAGACGCGGCTGCTGATCCACAGC 420  
QY 421 AGTGGCGGCTGGGCGGAACTTCAACAGCTCTATACGGGGACGGGGCCCTGAGAGACGCAAG 480  
DB 421 AGTGGGGGCTGGGCGGAGTTTCAACAGCTCTATACGGGGACGGGGCCCTGAGAGAGCGCGG 480  
QY 481 CGTCTGCGGAGGGAAGTGGGATGAGTGAAGCAAGTGTGACGGGGCGGTGGCACTG 540  
DB 481 CGTCTGCGGAGGGAAGTGGGATGAGTGAAGCAAGTGTGACGGGGCGGTGGCACTG 540  
QY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581  
DB 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581

RESULT 12

ABT16642  
ID ABT16642 standard; DNA; 3542 BP.

XX AC ABT16642;  
XX DT 03-APR-2003 (first entry)  
XX DE Human bcl-2 gene SEQ ID No 4.  
XX DE  
XX ANti-tumour; DNazyme; bcl-2 gene; tumour; malignant; chemotherapy;  
XX KW radiation therapy; catalytic domain; enzyme; human; ds.  
XX OS Homo sapiens.  
XX PN WO200299090-A1.  
XX PD 12-DEC-2002.  
XX PF 07-JUN-2002; 2002WO-AU000739.  
XX PR 07-JUN-2001; 2001AU-00005527.  
XX PA (JOHU ) JOHNSON & JOHNSON RES PTY LTD.  
XX

PI Sun L, Wang L, Turner RJ, Saravolac EG, Dass CR;  
XX DR WPI; 2003-140617/13.

XX Novel DNazyme useful for treating tumors, and for enhancing the  
PT sensitivity of malignant or virus infected cells to therapy, comprises a  
PT catalytic domain and binding domain contiguous to the catalytic domain.

XX Disclosure; Page 44-45; 67pp; English.

PS The invention relates to a DNazyme which specifically cleaves mRNA  
CC transcribed from a member of the bcl-2 gene family. The DNazymes comprise  
CC a catalytic domain, binding domains contiguous with the 5' and 3' end of  
CC the catalytic domain, and therefore hybridise with the two regions  
CC immediately flanking the purine residue of the cleavage site within the  
CC bcl-2 gene family mRNA, at which DNazyme-catalysed cleavage is desired. A  
CC pharmaceutical composition comprising a DNazyme of the invention is  
CC useful for treating tumors in a subject, and for enhancing the  
CC sensitivity of malignant or virus infected cells infected cells to  
CC therapy. The DNazymes are useful in diagnostics, therapeutics,  
CC prophylaxis, research agents and in kits. The DNazymes are also useful  
CC for increasing the susceptibility of tumour cells to anti-tumour  
CC therapies such as chemotherapy and radiation therapy. This polynucleotide  
CC sequence represents a human bcl-2 gene of the invention  
XX

SQ Sequence 3542 BP; 804 A; 817 C; 1030 G; 891 T; 0 U; 0 Other;  
Query Match 86.5%; Score 502.6; DB 8; Length 3542;  
Best Local Similarity 91.6%; Pred. No. 3e-126;  
Matches 532; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGCTTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
DB 177 ATGGCGACCCCAAGCTTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 236  
QY 61 AGGCTGAGGAGAGAGGTTATGTCTGTGAGAGCTGGGCTGGGGAAGGCCGAGCCGCGAC 120  
DB 237 AAGCTGAGGAGAGAGGTTATGTCTGTGAGAGCTGGGCTGGGGAAGGCCGAGCGACTGAC 296  
QY 121 CCGCTGACCAAGCCATGCGGGCTGTGAGAGCAAGTTTGAGACCCGTTCCGCGCACCC 180  
DB 297 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCCGCGCACCC 356  
QY 181 TTCTTGACCTGGCCGCTCAGCTACAGTGAAGCCAGGCTCAGGCCAGCAAGCCTTACC 240  
DB 357 TTCTTGATCTGGCGGCTCAGCTGATGATGAAGCCAGGCTCAGGCCAGCAAGCCTTACC 416  
QY 241 CAGGTTTCCGAGCAAGCTTTTCCAAAGGGGGCCCTAAGTGGGCGGCTTGTGCAATCTTT 300  
DB 417 CAGGTTTCCGAGCAAGCTTTTCCAAAGGGGGCCCAAGTGGGCGGCTTGTAGCCTTCTTT 476  
QY 301 GTCTTTGGGGCTGCCCTGTGTGTGAGAGTTCACAAAGAAATGAGCCTTTGGTGGA 360  
DB 477 GTCTTTGGGGCTGCACTGTGTGTGAGAGTTCACAAAGAGATGAAACCACTGGTGGA 536  
QY 361 CAAGTCCAGAGATTGATCGTGCGCTAAGTGAAGACACGCTGTGCTGATCCACAGC 420  
DB 537 CAAGTCCAGAGATGATGCTGCGCTAAGTGAAGACGCGGCTGTGCTGATCCACAGC 596  
QY 421 AGTGGCGGCTGGGCGGAACTTCAACAGCTCTATACGGGGACGGGGCCCTGAGAGCGCACGG 480  
DB 597 AGTGGGGGCTGGGCGGAGTTTCAACAGCTCTATACGGGGACGGGGCCCTGAGAGCGCGG 656  
QY 481 CGTCTGCGGAGGGAAGTGGGATGAGTGAAGCAAGTGTGAGCGGGCCGTGGCACTG 540  
DB 657 CGTCTGCGGAGGGAAGTGGGATGAGTGAAGCAAGTGTGAGCGGGCCGTGGCACTG 716  
QY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581  
DB 717 GGGGCCCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 757

RESULT 13

AAT96577  
ID AAT96577 standard; DNA; 583 BP.  
XX  
AC AAT96577;  
XX  
DT 22-APR-1998 (first entry)  
XX  
DE Human bcl-w DNA.  
XX  
KM Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
XX diagnosis; degenerative disease; ss.  
OS  
XX Homo sapiens.  
FH  
FT Key Location/Qualifiers  
FT CDS 1..582  
FT /\*tag= a  
FT /product= "bcl-w"  
XX  
PN WO9735971-A1.  
XX  
PD 02-OCT-1997.  
XX  
PF 27-MAR-1997; 97WO-AU000199.  
XX  
PR 27-MAR-1996; 96AU-00008965.  
XX  
PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX  
PI Cory S, Adams JM, Gibson LM, Holmgreen SP;  
XX  
DR WPI; 1997-489635/45.  
DR P-PSDB; AAW36047.  
XX  
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or  
PT inhibit cell survival, e.g. for treatment of cancer and degenerative  
XX diseases.  
XX  
PS Claim 3; Page 48; 86pp; English.  
XX  
CC This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene  
CC family, extracted from an adult brain library. This gene promotes cell  
CC survival, so its modulation is useful in treatment of cancer or auto-  
CC immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease,  
CC myocardial infarct, muscular degeneration, hypoxia, ischaemia, human  
CC immunodeficiency virus infection or in cell transplants. Up-regulation of  
CC the gene can also be used to modify cell lines cultured in vivo, e.g. to  
CC develop new lines, to facilitate isolation of hybridomas and to increase  
CC survival of primary explants during genetic modification. It can be used  
CC to produce recombinant Bcl-w for therapy, diagnosis, antibody production  
CC or screening of potential modulators  
XX  
SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;  
Query Match 86.2%; Score 501; DB 2; Length 583;  
Best Local Similarity 91.4%; Pred. No. 4.7e-126;  
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;  
QY 1 ATGCCGACCCCAAGCTTCAACCCAGACACAGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
Db 1 ATGGCGACCCCAAGCTTCAACCCAGACACAGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
QY 61 AGGCTGAGCAGAGAGGCTTATGTCTGTGAGAGCTGGGCTGGGGAAGGCCCAAGCCCGAC 120  
Db 61 AAGCTGAGCAGAGAGGCTTATGTCTGTGAGAGCTGGGCTGGGGAAGGCCCAAGCTGAC 120  
QY 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGCGAGTTTGAGACCCCGTTCCGCGCAGAC 180  
Db 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGCGAGTTTGAGACCCCGTTCCGCGCAGAC 180  
QY 181 TTCTTGACCTGGCGCTCAGCTACAGTACAGTACCCAGGCTCAGCCCAAGCGTTACAC 240  
Db 181 TTCTTGATCTGGCGCTCAGCTCAGTACAGTACCCAGGCTCAGCCCAAGCGTTACAC 240

QY 241 CAGTTTCCGACGAACTTTTCCAGGGGGCCCTTAACTGGGGCCGTTGTGCAATCTTT 300  
Db 241 CAGTTTCCGACGAACTTTTCAAGGGGGCCCACTGGGGCCGCTTGTAGCCTTCTT 300  
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QY 361 CAAGTCCAGGATTGATCGTGGCCTTACCTGAGACACAGTCTGACTGATCCACAGC 420  
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QY 421 AGTGGCGGCTGGCGGACTTCAACAGCTCTATACGGGGAGCGGGCCCTGAGACGCAAG 480  
Db 421 AGTGGGGCTGGCGGAGTTCAACAGCTCTATACGGGGAGCGGGCCCTGAGAGCGCGG 480  
QY 481 CGTCTGCGGAGGCACTGGGCAATGAGTGAGCACAGTGTGACGGGGCGGTGCACTG 540  
Db 481 CGTCTGCGGAGGGAAGTCAAGTCAAGTGAAGACAGTGTGACGGGGCGGTGCACTG 540  
QY 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTGTAAGTGTG 581  
Db 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTGTAAGTGTG 581

RESULT 14

AAX25134  
ID AAX25134 standard; DNA; 583 BP.  
XX  
AC AAX25134;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Human bcl-w gene derivative.  
XX  
KW Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;  
XX animal model; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9913710-A1.  
XX  
PD 25-MAR-1999.  
XX  
PF 16-SEP-1998; 98WO-AU000764.  
XX  
PR 16-SEP-1997; 97AU-00009228.  
XX  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX  
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;  
XX  
DR WPI; 1999-243890/20.  
DR P-PSDB; AAY05532.  
XX  
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
PT protein associated with Bcl-w.  
XX  
PS Disclosure; Page 36; 52pp; English.  
XX

The present sequence is described as a derivative of the human bcl-w gene (see AAX25132) and encodes Bcl-w protein (see AAY05532), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation in at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals have disorganised seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can

CC be used to screen for therapeutic molecules including genetic sequences  
CC capable of inducing, enhancing or otherwise facilitating spermatogenesis  
CC in animals, or which can induce infertility

XX Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;

Query Match 86.2%; Score 501; DB 2; Length 583;  
Best Local Similarity 91.4%; Pred. No. 4.7e-126;  
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

OY 1 ATGCCGACCCAGCCTCAACCCAGACACAGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
DB 1 ATGGCGACCCAGCCTCGGCCAGACACAGCGCTCTGTGGCAGACTTTGTAGGTTAT 60  
OY 61 AGGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGCCCTGGGAAGGCCAGCCGCCGAC 120  
DB 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGCCCGGAGAGGCCAGAGCTGAC 120  
OY 121 CCGCTGACCAAGCCATGCGGCTGTGAGACGAGTTTGAGACCCGTTCCGCCGAC 180  
DB 121 CCGCTGACCAAGCCATGCGGCTGTGAGACGAGTTTGAGACCCGTTCCGCCGAC 180  
OY 181 TTCTCTGACTGGCCGCTCAGCTACAGTGAACCCAGGCTCAGCCCAAGCAAGCTTACC 240  
DB 181 TTCTCTGACTGGCCGCTCAGCTCAGTGAACCCAGGCTCAGCCCAAGCAAGCTTACC 240  
OY 241 CAGGTTCCGACGAACCTTTCCAAAGGGGCGCTTAAGTGGGCGCTTGTGGCATTCCTT 300  
DB 241 CAGGTTCCGACGAACCTTTCCAAAGGGGCGCTTAAGTGGGCGCTTGTGGCATTCCTT 300  
OY 301 GTCTTTGGGCTGCCCTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCTTGTGGGA 360  
DB 301 GTCTTTGGGCTGCCCTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCTTGTGGGA 360  
OY 361 CAAGTCCAGATTTGATCGTGGCTTACCTGAGACACAGCTGTGCTGATCCACAGC 420  
DB 361 CAAGTCCAGATTTGATCGTGGCTTACCTGAGACACAGCTGTGCTGATCCACAGC 420  
OY 421 AGTGGCGCTGGCGGACTTACAGCTCTATACGGGGAGCGGGCCCTGGAGAGCAGCAG 480  
DB 421 AGTGGCGCTGGCGGACTTACAGCTCTATACGGGGAGCGGGCCCTGGAGAGCAGCAG 480  
OY 481 CGTTCGGGAGGGCACTGGGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540  
DB 481 CGTTCGGGAGGGCACTGGGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540  
OY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTG 581  
DB 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTG 581

RESULT 15  
AAV28334  
ID AAV28334 standard; cDNA; 579 BP.

AC AAV28334;  
XX  
DT 02-OCT-1998 (first entry)  
XX  
DE Human bcl-y gene.  
XX  
KW ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.  
XX  
OS Homo sapiens.  
XX

Key Location/Qualifiers  
FT CDS 1..579  
FT /tag= a  
FT /product= "bcl-y"  
FT /note= "No stop codon given"  
XX  
XX US5789201-A.  
XX

PD 04-AUG-1998.  
XX  
PF 11-FEB-1997; 97US-00798897.  
XX  
PR 23-FEB-1996; 96US-0012201P.  
XX  
PA (COCE-) COCENSYS INC.  
XX  
PI Guastella J;  
XX  
DR WPI; 1998-446079/38.  
DR P-PSDB; AAM61392.

PT Nucleic acids encoding B-cell lymphoma-y protein - useful for producing  
PT recombinant protein for use in treating uncontrolled cell growth e.g.  
PT cancers.  
XX  
PS Claim 3; Column 15/16; 27pp; English.

CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2  
CC family, components in the cell death pathway. The bcl-2 family have both  
CC apoptotic activity and the apoptosis blocking activity. bcl-y falls in  
CC the apoptosis activity category. The recombinant protein may be used to  
CC prevent uncontrolled cell growth, either by its direct administration to  
CC recombinant genetic constructs to increase its expression in vivo. Also,  
CC antisense constructs can be used in disorders where prevention of cell  
CC death is desired  
XX

SO Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 U; 0 Other;

Query Match 85.6%; Score 497.4; DB 2; Length 579;  
Best Local Similarity 91.2%; Pred. No. 4.5e-125;  
Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

OY 1 ATGCCGACCCAGCCTCAACCCAGACACAGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
DB 1 ATGGCGACCCAGCCTCGGCCAGACACAGCGCTCTGTGGAAGACTTTGTAGGTTAT 60  
OY 61 AGGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGCCGCCGAC 120  
DB 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGAGCTGAC 120  
OY 121 CCGCTGACCAAGCCATGCGGCTGTGAGACGAGTTTGAGACCCGTTCCGCCGAC 180  
DB 121 CCACTGACCAAGCCATGCGGCTGTGAGACGAGTTTGAGACCCGTTCCGCCGAC 180  
OY 181 TTCTCTGACTGGCCGCTCAGCTTACAGTGAACCCAGGCTCAGCCCAAGCAAGCTTACC 240  
DB 181 TTCTCTGACTGGCCGCTCAGCTTACAGTGAACCCAGGCTCAGCCCAAGCAAGCTTACC 240  
OY 241 CAGGTTCCGACGAACCTTTCCAAAGGGGCGCTTAAGTGGGCGCTTGTGGCATTCCTT 300  
DB 241 CAGGTTCCGATGAACCTTTTCAAGGGGCGCCCAACTGGGCGCTTGTAGCCTTCTT 300  
OY 301 GTCTTTGGGCTGCCCTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCTTGTGGGA 360  
DB 301 GTCTTTGGGCTGCCCTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCTTGTGGGA 360  
OY 361 CAAGTCCAGATTTGATCGTGGCTTACCTGAGACACAGCTGTGCTGACTGATCCACAGC 420  
DB 361 CAAGTCCAGATTTGATCGTGGCTTACCTGAGACACAGCTGTGCTGACTGATCCACAGC 420  
OY 421 AGTGGCGCTGGCGGACTTACAGCTCTATACGGGGAGCGGGCCCTGGAGAGCAGCAG 480  
DB 421 AGTGGCGCTGGCGGAGTTTACAGCTCTATACGGGGAGCGGGCCCTGGAGAGCAGCAG 480  
OY 481 CGTTCGGGAGGGCACTGGGCATGAGTGAGCAGAGTGTGACGGGGCCGTGGCACTG 540  
DB 481 CGTTCGGGAGGGCACTGGGCATGAGTGAGCAGAGTGTGACGGGGCCGTGGCACTG 540  
OY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAG 579  
DB 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTCTAGCAAG 579

Mon Apr 11 12:21:54 2005

Search completed: April 10, 2005, 16:55:36  
Job time : 457.215 secs

us-09-925-674b-8.rng

Page 12



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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 16:31:16 ; Search time 143.753 Seconds  
(without alignments)  
6613.285 Million cell updates/sec

Title: US-09-925-674B-8

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	581	100.0	581	4	US-09-155-327G-8 Sequence 8, Appli
2	540.6	93.0	579	1	US-08-798-897-1 Sequence 1, Appli
3	540.6	93.0	579	2	US-08-978-523-1 Sequence 1, Appli
4	501	86.2	582	4	US-09-949-016-5057 Sequence 5057, Ap
5	501	86.2	583	4	US-09-155-327G-6 Sequence 6, Appli
6	497.4	85.6	579	1	US-08-798-897-2 Sequence 2, Appli
7	497.4	85.6	579	2	US-08-978-523-2 Sequence 2, Appli
8	364.8	62.8	1098	4	US-09-010-147B-23 Sequence 23, Appl
9	364.4	62.7	1864	3	US-09-149-476-130 Sequence 130, App
10	364.2	62.7	5199	4	US-09-949-016-16799 Sequence 16799, A
11	357	61.4	601	4	US-09-949-016-177003 Sequence 177003,
12	134.6	23.2	926	1	US-08-081-448-5 Sequence 5, Appli
13	134.6	23.2	926	2	US-08-470-670A-6 Sequence 6, Appli
14	134.6	23.2	926	3	US-08-481-739-1 Sequence 1, Appli
15	134.6	23.2	926	3	US-09-167-921-1 Sequence 1, Appli
16	134.6	23.2	926	3	US-09-277-020-39 Sequence 39, Appl
17	134.6	23.2	926	3	US-09-323-743-1 Sequence 1, Appli
18	134.6	23.2	926	3	US-08-461-511A-6 Sequence 6, Appli
19	134.6	23.2	926	3	US-09-271-014A-5 Sequence 5, Appli
20	134.6	23.2	926	4	US-09-023-655-1430 Sequence 1430, Ap
21	134.6	23.2	926	4	US-09-814-915A-106 Sequence 106, App
22	134.6	23.2	926	5	PCT-US94-07089-6 Sequence 6, Appli
23	134.6	23.2	1236	4	US-09-639-245-1 Sequence 1, Appli
24	130.6	22.5	1455	4	US-09-639-245-7 Sequence 7, Appli
25	126.8	21.8	60489	4	US-09-949-016-16287 Sequence 16287, A
26	125	21.5	717	2	US-08-465-485A-20 Sequence 20, Appl
27	125	21.5	717	3	US-09-080-285-20 Sequence 20, Appl

28	125	21.5	4825	6	5459251-1	Patent No. 5459251
29	125	21.5	4825	6	5459251-1	Patent No. 5459251
30	125	21.5	5086	2	US-08-465-485A-19	Sequence 19, Appl
31	125	21.5	5086	2	US-08-365-486A-14	Sequence 14, Appl
32	125	21.5	5086	3	US-09-080-285-19	Sequence 19, Appl
33	125	21.5	5086	3	US-08-880-342-14	Sequence 14, Appl
34	125	21.5	5086	3	US-09-724-426-19	Sequence 19, Appl
35	125	21.5	5086	3	US-09-233-527-7	Sequence 7, Appli
36	125	21.5	5086	5	PCT-US93-05651-4	Sequence 4, Appli
37	125	21.5	5086	5	PCT-US93-06251-2	Sequence 2, Appli
38	125	21.5	5094	3	US-09-234-186-7	Sequence 7, Appli
39	125	21.5	5104	6	5506344-1	Patent No. 5506344
40	125	21.5	5104	6	5506344-1	Patent No. 5506344
41	125	21.5	6030	4	US-09-023-655-1015	Sequence 1015, Ap
42	123.4	21.2	760	1	US-08-405-702A-11	Sequence 11, Appl
43	123.4	21.2	1846	2	US-08-365-486A-16	Sequence 16, Appl
44	123.4	21.2	1846	3	US-08-880-342-16	Sequence 16, Appl
45	121.8	21.0	711	4	US-09-741-238-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-09-155-327G-8  
Sequence 8, Application US/09155327G  
Patent No. 6790637  
GENERAL INFORMATION:  
APPLICANT: AMRAD Operations Pty Ltd  
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2  
FILE REFERENCE: 2096584  
CURRENT APPLICATION NUMBER: US/09/155,327G  
CURRENT FILING DATE: 1999-03-29  
PRIOR APPLICATION NUMBER: PN8965  
PRIOR FILING DATE: 1996-03-27  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 581  
TYPE: DNA  
ORGANISM: Mouse  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(579)  
US-09-155-327G-8

Query Match	100.0%;	Score 581;	DB 4;	Length 581;
Best Local Similarity	100.0%;	Pred. No. 7.5e-162;		
Matches 581;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGCCGACCCAGCCTCAACCCAGACACACGCGCTAGTGGCTACTTTGTAGGCTAT	60	
DB	1	ATGCCGACCCAGCCTCAACCCAGACACACGCGCTAGTGGCTACTTTGTAGGCTAT	60	
QY	61	AGGCTGAGGAGAGAGGTTATGTTGAGAGCTGGGCTGGGAGAGGCCAGCCGCGAC	120	
DB	61	AGGCTGAGGAGAGAGGTTATGTTGAGAGCTGGGCTGGGAGAGGCCAGCCGCGAC	120	
QY	121	CCGCTGACCAAGCCATGCGGCTGCTGAGAGAGTTGAGACCCGTTCCGCGCACC	180	
DB	121	CCGCTGACCAAGCCATGCGGCTGCTGAGAGAGTTGAGACCCGTTCCGCGCACC	180	
QY	181	TTCTCTGACCTGGCCGCTCAGCTACAGTGACCCAGGCTCAGCCAGCAAGCTTCAAC	240	
DB	181	TTCTCTGACCTGGCCGCTCAGCTACAGTGACCCAGGCTCAGCCAGCAAGCTTCAAC	240	
QY	241	CAGGTTTCCGACGAAGTTTCCAGAGGGGCTTAAGTGGGCGCTTGTGGCATTTCTTT	300	
DB	241	CAGGTTTCCGACGAAGTTTCCAGAGGGGCTTAAGTGGGCGCTTGTGGCATTTCTTT	300	
QY	301	GTCCTTGGGGCTGCCCTGTGTGCTGAGAGTCAACAAAGAAATGAGCCTTTGGTGGGA	360	

Db 301 GTCTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAATGAGAGCCTTTGGTGGGA 360  
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Db 421 AGTGGCGGCTGGGGGCACTTCACAGCTCTATACGGGGGACGGGGCCCTGGAGAGACGACGG 480  
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Db 481 CGTCTGCGGAGGGCACTGGGCATGAGTGAGCACAGTGTGACGGGGCCGTGGCACTG 540  
QY 541 GGGGCCCTGTAACTGTAGGGCCCTTTTGTCTAGCAAGTG 581  
Db 541 GGGGCCCTGTAACTGTAGGGCCCTTTTGTCTAGCAAGTG 581

RESULT 2  
US-08-798-897-1  
; Sequence 1, Application US/08798897  
; Patent No. 5789201  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 579 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
; US-08-798-897-1

Query Match 93.0%; Score 540.6; DB 1; Length 579;  
Best Local Similarity 95.9%; Pred. No. 6.6e-150;  
Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
QY 1 ATGCCGACCCAGCCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
Db 1 ATGGCGACCCAGCCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
QY 61 AGGCTGAGGACAGAGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGCCGCCGAC 120  
Db 61 AAGCTGAGACAGAGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGCCGCCGAC 120  
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QY 181 TTCTTGACTGGCCGCTCAGCTACAGTGACCCAGGCTCAGCCGACCAACGCTTACC 240  
Db 181 TTCTTGACTGGCCGCTCAGCTACAGTGACCCAGGCTCAGCCGACCAACGCTTACC 240  
QY 241 CAGGTTCCGACGAACCTTTTCCAAAGGGGCCCTAACTGGGGCCGCTTGTGGCATCTTT 300  
Db 241 CAGGTTCCGACGAACCTTTTCCAAAGGGGCCCCCAACTGGGGCCGCTTGTGGCATCTTT 300  
QY 301 GTCTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAATGAGACCTTTGGTGGGA 360  
Db 301 GTCTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAATGAGACCTTTGGTGGGA 360  
QY 361 CAAGTCCAGGATGGATTCGTGGCCCTACCTGGAGACACAGTCTGGCTGATCCACAGC 420  
Db 361 CAAGTCCAGGATGGATTCGTGGCCCTACCTGGAGACACAGTCTGGCTGATCCACAGC 420  
QY 421 AGTGGCGGCTGGGGGCACTTCACAGCTCTATACGGGGGACGGGGCCCTGGAGACGACGG 480  
Db 421 AGTGGGGGCTGGGGGCACTTCACAGCTCTATACGGGGGACGGGGCCCTGGAGACGACGG 480  
QY 481 CGTCTGCGGAGGGCACTGGGCATGAGTGAGCACACAGTGTGACGGGGCCGTGGCACTG 540  
Db 481 CGTCTGCGGAGGGCACTGGGCATGAGTGAGCACACAGTGTGACGGGGCCGTGGCACTG 540  
QY 541 GGGGCCCTGTAACTGTAGGGCCCTTTTGTCTAGCAAG 579  
Db 541 GGGGCCCTGTAACTGTAGGGCCCTTTTGTCTAGCAAG 579

RESULT 3  
US-08-978-523-1  
; Sequence 1, Application US/08978523  
; Patent No. 5883229  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/978,523  
; FILING DATE: herewith  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/798,897  
; FILING DATE: February 11, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 579 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both

TOPOLOGY: both  
MOLECULE TYPE: cDNA  
US-08-978-523-1

Query Match 93.0%; Score 540.6; DB 2; Length 579;  
Best Local Similarity 95.9%; Pred. No. 6.6e-150;  
Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGCTTCAACCCAGACACACGCGCTCTAGTGCTGCTTTGTAGGCTAT 60  
DB 1 ATGGCCGACCCCAAGCTTCAACCCAGACACACGCGCTCTAGTGCTGCTTTGTAGGCTAT 60  
QY 61 AGGCTGAGGAGAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGCCGCGAC 120  
DB 61 AAGCTGAGAGAGAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGCCGCGAC 120  
QY 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGAGTTGAGACCCGTTCCGCGCAC 180  
DB 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGAGTTGAGACCCGTTCCGCGCAC 180  
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DB 181 TTCTGTGACCTGGCGCTCAGCTACAGTGAAGCCAGGCTCAGCCAGCAAGCTTCAAC 240  
QY 241 CAGGTTCCGACGAATTTTCCAAAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCTT 300  
DB 241 CAGGTTCCGACGAATTTTCCAAAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCTT 300  
QY 301 GTCTTTGGGGCTGCGCTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCCTTTGGTGGGA 360  
DB 301 GTCTTTGGGGCTGCGCTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCCTTTGGTGGGA 360  
QY 361 CAAGTCCAGGATTTGATCGTGGCTTACCTGAGACAGCTGTGCTGATGATCCACAGC 420  
DB 361 CAAGTCCAGGATTTGATCGTGGCTTACCTGAGACAGCTGTGCTGATGATCCACAGC 420  
QY 421 AGTGGCGGCTGGCGGACTTCAAGCTCTAATACGGGGAAGGGGCGCTGAGAGACGACGG 480  
DB 421 AGTGGCGGCTGGCGGACTTCAAGCTCTAATACGGGGAAGGGGCGCTGAGAGACGACGG 480  
QY 481 CGTCTGCGGAGGGCAACTGGGCATGATGAGACAGAGTGTGACGGGGCGCTGTGGCACTG 540  
DB 481 CGTCTGCGGAGGGGAAGTGGGCATGATGAGAGACAGTGTGACGGGGCGCTGTGGCACTG 540  
QY 541 GGGGCGCTGTGTAAGTGTAGGGGCTTTTGTCTAGCAAG 579  
DB 541 GGGGCGCTGTGTAAGTGTAGGGGCTTTTGTCTAGCAAG 579

## RESULT 4

US-09-949-016-5057  
Sequence 5057, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5057  
LENGTH: 582  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-5057

Query Match 86.2%; Score 501; DB 4; Length 582;  
Best Local Similarity 91.4%; Pred. No. 3.4e-138;  
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGCTTCAACCCAGACACGCGCTCTAGTGCTGCTTTGTAGGCTAT 60  
DB 1 ATGGCCGACCCCAAGCTTCAACCCAGACACGCGCTCTAGTGCTGCTTTGTAGGCTAT 60  
QY 61 AGGCTGAGGAGAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGCCGCGAC 120  
DB 61 AAGCTGAGGAGAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGCCGCGAC 120  
QY 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGAGTTGAGACCCGTTCCGCGCAC 180  
DB 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGAGTTGAGACCCGTTCCGCGCAC 180  
QY 181 TTCTGTGACCTGGCGCTCAGCTACAGTGAAGCCAGGCTCAGCCAGCAAGCTTCAAC 240  
DB 181 TTCTGTGACCTGGCGCTCAGCTACAGTGAAGCCAGGCTCAGCCAGCAAGCTTCAAC 240  
QY 241 CAGGTTCCGACGAATTTTCCAAAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCTT 300  
DB 241 CAGGTTCCGACGAATTTTCCAAAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCTT 300  
QY 301 GTCTTTGGGGCTGCGCTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCCTTTGGTGGGA 360  
DB 301 GTCTTTGGGGCTGCGCTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCCTTTGGTGGGA 360  
QY 361 CAAGTCCAGGATTTGATCGTGGCTTACCTGAGACAGCTGTGCTGATGATCCACAGC 420  
DB 361 CAAGTCCAGGATTTGATCGTGGCTTACCTGAGACAGCTGTGCTGATGATCCACAGC 420  
QY 421 AGTGGCGGCTGGCGGACTTCAAGCTCTAATACGGGGAAGGGGCGCTGAGAGACGACGG 480  
DB 421 AGTGGCGGCTGGCGGACTTCAAGCTCTAATACGGGGAAGGGGCGCTGAGAGACGACGG 480  
QY 481 CGTCTGCGGAGGGCAACTGGGCATGATGAGACAGTGTGACGGGGCGCTGTGGCACTG 540  
DB 481 CGTCTGCGGAGGGGAAGTGGGCATGATGAGAGACAGTGTGACGGGGCGCTGTGGCACTG 540  
QY 541 GGGGCGCTGTGTAAGTGTAGGGGCTTTTGTCTAGCAAGTG 581  
DB 541 GGGGCGCTGTGTAAGTGTAGGGGCTTTTGTCTAGCAAGTG 581

## RESULT 5

US-09-155-327G-6  
Sequence 6, Application US/09155327G  
Patent No. 6790637  
GENERAL INFORMATION:  
APPLICANT: AMRAD Operations Pty Ltd  
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2  
TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES  
FILE REFERENCE: 2096584  
CURRENT APPLICATION NUMBER: US/09/155,327G  
CURRENT FILING DATE: 1999-03-29  
PRIOR APPLICATION NUMBER: PN8965  
PRIOR FILING DATE: 1996-03-27  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 583  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(579)  
US-09-155-327G-6

Query Match 86.2%; Score 501; DB 4; Length 583;  
Best Local Similarity 91.4%; Pred. No. 3.4e-138;  
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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QY 1 ATGCCGACCCCAAGCTTCAACCCAGACACACGCGCTTAGTGCTGACTTTGTAGCTAT 60
Db 1 ATGGCGACCCCAAGCTTCCGCCCCAGACACACGCGCTTAGTGCTGACTTTGTAGCTAT 60
QY 61 AGGCTGAGCAGAAAGGTTATGTCTGTGAGAGCTGGGCTGGGGAAGGCCAGCCGCCGAC 120
Db 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGAGCTGGGCTGGGGAAGGCCAGCCGCCGAC 120
QY 121 CCGCTGCACCAAGCCATGCGGGCTGTGAGACGAGTTGAGACCCGTTCCGCCGAC 180
Db 121 CCGCTGCACCAAGCCATGCGGGCTGTGAGAGATGAGTTGAGACCCGCTCCGCCGAC 180
QY 181 TTCTGTGACCTGGCCGCTCAGCTACAGTACCCAGCTCAGCCAGCAAGCTTACC 240
Db 181 TTCTGTGATCTGGCGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTACC 240
QY 241 CAGGTTCCGACGAACTTTTCAAGGGGCTTAAGTGGGCGCTTGTGGCATTTCTT 300
Db 241 CAGGTTCCGACGAACTTTTCAAGGGGCTTAAGTGGGCGCTTGTAGCCTTCTT 300
QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAAAAGAAATGAGCCTTTGGTGG 360
Db 301 CTCTTTGGGGCTGACCTGTGTGCTGAGAGTGTCAAAAGAGATGGAACCACTGTGG 360
QY 361 CAAGTCCAGGATTTGATCGTGCGCTACCTGAGACACGCTCTGCTGATCCACAGC 420
Db 361 CAAGTCCAGGATTTGATCGTGCGCTACCTGAGACACGCGCTGCTGATCCACAGC 420
QY 421 AGTGGCGGCTGGCGGCACTTACAGCTTATACGGGGACGGGCGCTGAGAGCGCACGG 480
Db 421 AGTGGGGGCTGGCGGCACTTACAGCTTATACGGGGACGGGCGCTGAGAGCGCGG 480
QY 481 CGTCTGCGGAGGCAACTGGGCAATGAGACAGTGTGACGGGGCGCTGGGCACTG 540
Db 481 CGTCTGCGGAGGGAAGTGGGCAATGAGAGACAGTGTGACGGGGCGCTGGGCACTG 540
QY 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTG 581
Db 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTG 581

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RESULT 6

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US-08-798-897-2
; Sequence 2, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600

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; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-08-798-897-2

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Query Match      85.6%; Score 497.4; DB 1; Length 579;
Best Local Similarity 91.2%; Pred. No. 3.9e-137;
Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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QY 1 ATGCCGACCCCAAGCTTCAACCCAGACACACGCGCTTAGTGCTGACTTTGTAGCTAT 60
Db 1 ATGGCGACCCCAAGCTTCCGCCCCAGACACACGCGCTTAGTGCTGACTTTGTAGCTAT 60
QY 61 AGGCTGAGCAGAAAGGTTATGTCTGTGAGAGCTGGGCTGGGGAAGGCCAGCCGCCGAC 120
Db 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGAGCTGGGCTGGGGAAGGCCAGCCGCCGAC 120
QY 121 CCGCTGCACCAAGCCATGCGGGCTGTGAGACGAGTTGAGACCCGTTCCGCCGAC 180
Db 121 CCGCTGCACCAAGCCATGCGGGCTGTGAGAGATGAGTTGAGACCCGCTCCGCCGAC 180
QY 181 TTCTGTGACCTGGCCGCTCAGCTACAGTACCCAGCTCAGCCAGCAAGCTTACC 240
Db 181 TTCTGTGATCTGGCGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTACC 240
QY 241 CAGGTTCCGACGAACTTTTCAAGGGGCTTAAGTGGGCGCTTGTGGCATTTCTT 300
Db 241 CAGGTTCCGACGAACTTTTCAAGGGGCTTAAGTGGGCGCTTGTAGCCTTCTT 300
QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAAAAGAAATGAGCCTTTGGTGG 360
Db 301 GTCTTTGGGGCTGACCTGTGTGCTGAGAGTGTCAAAAGAGATGGAACCACTGTGG 360
QY 361 CAAGTCCAGGATTTGATCGTGCGCTACCTGAGACACGCTCTGCTGATCCACAGC 420
Db 361 CAAGTCCAGGATTTGATCGTGCGCTACCTGAGACACGCGCTGCTGATCCACAGC 420
QY 421 AGTGGCGGCTGGCGGCACTTACAGCTTATACGGGGACGGGCGCTGAGAGCGCACGG 480
Db 421 AGTGGGGGCTGGCGGCACTTACAGCTTATACGGGGACGGGCGCTGAGAGCGCGG 480
QY 481 CGTCTGCGGAGGCAACTGGGCAATGAGACAGTGTGACGGGGCGCTGGGCACTG 540
Db 481 CGTCTGCGGAGGGAAGTGGGCAATGAGAGACAGTGTGACGGGGCGCTGGGCACTG 540
QY 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAAG 579
Db 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAAG 579

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RESULT 7

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US-08-978-523-2
; Sequence 2, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,523  
FILING DATE: herewith  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 579 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
US-08-978-523-2

Query Match 85.6%; Score 497.4; DB 2; Length 579;  
Best Local Similarity 91.2%; Pred. No. 3.9e-137;  
Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGCCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
DB 1 ATGCCGACCCCAAGCCTCGGCCCCAGACACACGCGCTCTGTGGAAGACTTTGTAGGTTAT 60  
QY 61 AGCTGAGGAGAGAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCCAAGCCCGAC 120  
DB 61 AAGCTGAGGAGAGAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCCAAGCTGAC 120  
QY 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGACGAGTTGAGACCCGTTTCCGCGCAC 180  
DB 121 CCACTGACCAAGCCATGCGGCTGTGAGAGATGAGTTCGAGACCCGCTTCCGCGCAC 180  
QY 181 TTCTCTGACCTGGCGCTCAGCTACAGCTGACCCCAAGGCTCAGCCCAACAGCTTACC 240  
DB 181 TTCTCTGATCTGGCGCTCAGCTGATGATGACCCCAAGGCTCAGCCCAACAGCTTACC 240  
QY 241 CAGGTTCCGACGAACCTTTCCAAAGGGGCTTAAGTGGGCGGCTTGTGGCATTTCTT 300  
DB 241 CAGGTTCCGATGAACCTTTTCAAGGGGCTTAAGTGGGCGGCTTGTAGCTTTCTT 300  
QY 301 GTCTTTGGGGCTGCCCTGTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCTTTGGTGG 360  
DB 301 GTCTTTGGGGCTGCCCTGTGTGTGCTGAGAGTGTCAACAAAGAGATGAACTGTGGGA 360  
QY 361 CAAGTCCAGATGATGATGCTGAGCTTACCTGAGACACGCTGTGGCTGATCCACAGC 420  
DB 361 CAAGTCCAGAGATGATGCTGAGCTTACCTGAGACACGCTGTGGCTGATCCACAGC 420  
QY 421 AGTGGCGCTGGCGGACTTCAAGCTCTAATACGGGACGGGCGCTTGAAGACGACCG 480  
DB 421 AGTGGCGCTGGCGGACTTCAAGCTCTAATACGGGACGGGCGCTTGAAGAGCGCG 480  
QY 481 CGTCTGCGGAGGAGCACTGGGATGAGTGAACAGTGTGACGGGCGCTTGGCACTG 540  
DB 481 CGTCTGCGGAGGAGCACTGGGATGAGTGAACAGTGTGACGGGCGCTTGGCACTG 540  
QY 541 GGGGCGCTGTAACTGTAGGGGCTTTTGTAGCAAG 579  
DB 541 GGGGCGCTGTAACTGTAGGGGCTTTTGTAGCAAG 579

RESULT 8

US-09-010-147B-23  
Sequence 23, Application US/09010147B  
Patent No. 6653445  
GENERAL INFORMATION:  
APPLICANT: N1 et al.  
TITLE OF INVENTION: Human Proteins  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC  
compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/010,147B  
FILING DATE: 12-No. 6653445-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,205  
FILING DATE: 21-JAN-1997  
APPLICATION NUMBER: US 60/034,204  
FILING DATE: 21-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Jonathan J. Klein  
REGISTRATION NUMBER: 41,119  
REFERENCE/DOCKET NUMBER: PF353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1098 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1095  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-010-147B-23

Query Match 62.8%; Score 364.8; DB 4; Length 1098;  
Best Local Similarity 90.3%; Pred. No. 8.2e-98;  
Matches 390; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGCCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
DB 1 ATGCCGACCCCAAGCCTCGGCCCCAGACACACGCGCTCTGTGGAAGACTTTGTAGGTTAT 60  
QY 61 AGCTGAGGAGAGAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCCAAGCCCGAC 120  
DB 61 AAGCTGAGGAGAGAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCCAAGCTGAC 120  
QY 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGACGAGTTTGAAGCCGTTTCCGCGCAC 180  
DB 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGATGAGTTCGAGACCCGCTTCCGCGCAC 180  
QY 181 TTCTCTGACCTGGCGCTCAGCTACAGCTGACCCCAAGGCTCAGCCCAACAGCTTACC 240  
DB 181 TTCTCTGATCTGGCGCTCAGCTGATGATGACCCCAAGGCTCAGCCCAACAGCTTACC 240  
QY 241 CAGGTTCCGACGAACCTTTCCAAAGGGGCTTAAGTGGGCGGCTTGTGGCATTTCTT 300  
DB 241 CAGGTTCCGATGAACCTTTTCAAGGGGCTTAAGTGGGCGGCTTGTAGCTTTCTT 300



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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Query Match 62.7%; Score 364.4; DB 3; Length 1864;  
 Best Local Similarity 90.0%; Pred. No. 1.4e-97;  
 Matches 389; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

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QY 1 ATGCCGACCCCAACCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
DB 11 ATGGCAGCCCAAGCTCGGCCAGACACACGCGCTCTGTTGGCAGACTTTGTAGGTTAT 70
QY 61 AGGCTGAGGAGAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGCCCGGAC 120
DB 71 AAGCTGAGGAGAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGAGCTGAC 130
QY 121 CCGCTGACCAAGCCATGCGGCTGTGAGACGAGTTTGAGACCCGTTCCCGCGAC 180
DB 131 CCGCTGACCAAGCCATGCGGCTGTGAGACGAGTTTGAGACCCGTTCCCGCGAC 190
QY 181 TTCTTGACCTGGCCGCTCAGCTACGTCAGCCAGGCTCAGCCGCAAGCCTTACC 240
DB 191 TTCTTGATCTGGCGGCTCAGCTCAGTCAGTCAGCCAGGCTCAGCCGCAAGCCTTACC 250
QY 241 CAGTTTCCGACGAACCTTTCCAGAGGGGCCCTTAAGTGGGCGGCTTGTGCTATTCTT 300
DB 251 CAGTTTCCGACGAACCTTTCCAGAGGGGCCCTTAAGTGGGCGGCTTGTGCTATTCTT 310
QY 301 GTCTTTGGGCTGCCCTGTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCTTTGTGGA 360
DB 311 GTCTTTGGGCTGCACTGTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCTTTGTGGA 370
QY 361 CAAGTCCAGATTGATGCTGTGCTTACCTGAGACACAGCTGTGCTGATCCAGC 420
DB 371 CAAGTCCAGATTGATGCTGTGCTTACCTGAGACACAGCTGTGCTGATCCAGC 430
QY 421 AGTGGGCGCTGG 432
DB 431 AGTGGGCGCTGG 442

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RESULT 10  
 US-09-949-016-16799  
 ; Sequence 16799, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 16799  
 ; LENGTH: 5199  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-16799

Query Match 62.7%; Score 364.2; DB 4; Length 5199;  
 Best Local Similarity 90.1%; Pred. No. 2.4e-97;  
 Matches 390; Conservative 0; Mismatches 43; Indels 0; Gaps 0;  
 QY 1 ATGCCGACCCCAAGCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
 DB 2001 ATGGCAGCCCAAGCTCGGCCAGACACACGCGCTCTGTTGGCAGACTTTGTAGGTTAT 2060  
 QY 61 AGGCTGAGGAGAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGCCCGGAC 120  
 DB 2061 AAGCTGAGGAGAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGAGCTGAC 2120  
 QY 121 CCGCTGACCAAGCCATGCGGCTGTGAGACGAGTTTGAGACCCGTTCCCGCGCACC 180

us-09-925-674b-8.rtf

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Db	361	CAAGTCAGAGATTGATCGTGCCTTACTGTGAGAGTGTCAACACAGAGATGGAACCACTGTTGGA
QY	539	CAAGTCAGAGAGTGTGATGTGTGCTTACTGTGAGACACAGCTGTGCTGACTGTGATCCACAGC
Db	421	AGT 423
QY	421	AGT 423
Db	599	AGT 601
QY	599	AGT 601
RESULT 12		
US-08-081-448-5		
/ Sequence 5		
/ Page 1		

RESULT 12  
 US-08-081-448-5  
 ; Sequence 5, Application US/08081448  
 ; Patent No. 5646008  
 ; GENERAL INFORMATION  
 ; APPLICANT: Thompson, Craig B.  
 ; APPLICANT: Boise, Lawrence H.  
 ; TITLE OF INVENTION: Vertebrate Apoptosis Gene:  
 ; NUMBER OF INVENTION: Compositions and Methods  
 ; CORRESPONDENCE ADDRESSES: 8  
 ; ADDRESS: Arnold, White & Durkee  
 ; STREET: 321 No. 5646008th Clark Street, Suite 800  
 ; CITY: Chicago  
 ; STATE: IL  
 ; COUNTRY: USA  
 ; ZIP: 60610  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/081,448  
 ; FILING DATE: 19930622  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: No. 5646008thrup, Thomas E.  
 ; REGISTRATION NUMBER: 33,268  
 ; REFERENCE/DOCKET NUMBER: ARCD090  
 ; TELEPHONE: 312-744-0090  
 ; TELEFAX: 312-755-4489  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 926 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 135..836  
 ; US-08-081-448-5

Query Match	Best Local Matches	Similarity	Score	DB	Length
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236	Conservative	0	Mismatches	169	Indels
0	Gaps	0			
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Qy	394	AGCAAGCGCTGAGGAGCGAGCCGACGAGTTTGAATCGCGTACCGCGGCATTCTTG			
Db	188	ACCTGGCGGCTAGCTACACGTGAACCCAGGCTCAGCCAGCAACGTTTACCACCGATT			
Qy	454	ACCTGACATCCAGCTCCACATCACCACGAGGACAGCATATCAGAGCTTTGAACAGTTAG			
Db	248	CCGACGAATTTTCCAAAGGGGCGCCTAACTGGGGCGGCTTGTGCAATCTTTGTCTTGG			
Qy	514	TGATGAACTTTCGGGATGGGGTAACCTGGGGTGCATTGTGGCCTTTTCTCCTTGC			



OY		308	G G G C T G C C C T G T G T G C T G A G A G T G T C A C A A A G A A T G G A G C C T T T G G T G G G A C A A G T C C	367
D b		574	G C G G G C A C T G T G C G T G A A A G C G T A G A C A G A G A T G C A G G T A T T G G T G A G T C G A T C G	633
OY		368	A G A T T G A T C G T G G C C T A C C T G A G A C A C G T C T G A C T G A T C C A C A G C A G T G C G	427
D b		634	C A G C T T G G A T G G C C A C T T A C C T G A T G A C C A C C T T A G A G C C T T G G A T C C A G A G A A C G G C G	693
OY		428	G C T G G C G G A C T T C A C A G C T T A T A C G G G A C G G G G C C C T G A G A G A C G A C G G C G T C G C	487
D b		694	G C T G G S A T A C T T T T G T G G A C T C T A T G G A C A A T G C A G A C C G A G A G C C G A A A G G G C C	753
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D b		754	A G G A A C G C T T C A A C C G C T G T T C C T G A C C G G G C A T G A C T G T G C C G	798

## RESULT 13

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Sequence 6, Application US/08470670A
Patent No. 5834309
Patent No. 5834309 5710045
GENERAL INFORMATION:
APPLICANT: Thompson, Craig B. B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,670A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,448
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:090--1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 135..836
US-08-470-670A-6

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Query Match	23.2%;	Score 134.6;	DB 2;	Length 926;
Best Local Similarity	58.3%;	Pred. No. 8.8e-30;		
Matches 236;	Conservative 0;	Mismatches 169;	Indels 0;	Gaps 0;

QY 128 ACCAAGCCATGCGGGCTGTCTGAGACGATTTGAGACCCTTTCGCCGCACCTTTCTG 187  
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Db 394 AGCAAGCGCTGAGGGAGGACGCGCAGAGTTTGAACTGCGGTACCGGCGGGCATTTCACTG 453

[illegible]

## RESULT 14

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: Sequence 1, Application US/08481739
: Patent No. 6143291
: GENERAL INFORMATION:
: APPLICANT: June, Carl H. and Thompson, Craig B.
: TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
: TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD
: STREET: 28 State Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/481,739
: FILING DATE: 07-JUNE-1995
: PRIOR APPLICATION NUMBER: US 08/435,518
: FILING DATE: 04-MAY-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: DeConti, Giulio A. (GAD)
: REGISTRATION NUMBER: 31,503
: REFERENCE/DOCKET NUMBER: RPI-034CP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)742-4214
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 926 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 135..836
:
: US-08-481-739-1

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Query Match	23.2%	Score 134.6;	DB 3;	Length 926;
Best Local Similarity	58.3%	Pred. No. 8.8e-30;		

Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

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QY 188 ACCTGGCGGCTCAGCTACACGTGACCCCGAGGCTCAGCCGACGACGCTTCAACCAAGTTT 247
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QY 308 GGGCTGCCCTGTGTCTGCTGAGAGTGTCAACAAGAAATGAGCCCTTGGTGGGACAAAGTCC 367
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RESULT 15

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US-09-167-921-1
; Sequence 1, Application US/09167921A
; Patent No. 6172216
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, QingQing
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0324
; CURRENT APPLICATION NUMBER: US/09/167,921A
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(836)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: L20121 Genbank
; DATABASE ENTRY DATE: 1994-07-26
US-09-167-921-1

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Query Match 23.2%; Score 134.6; DB 3; Length 926;  
 Best Local Similarity 58.3%; Pred. No. 8.8e-30;  
 Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

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QY 128 ACCAAGCCATGCGGGCTGCTGAGACGAGTTTGAGACCCGTTTCCGCCGACCTTCTCTG 187
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QY 248 CCGACGAACCTTTCCAAAGGGGCGCTTAAGTGGGCGGCTTGTGTCATCTTGTCTTGTG 307
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Db 514 TGAATGAACCTTCCCGGATGGGCTAAACTGGGCTCGCATTTGTGGCTTTTCTCTCTG 573
QY 308 GGGCTGCCCTGTGTCTGCTGAGAGTGTCAACAAGAAATGAGCCCTTGGTGGGACAAAGTCC 367
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Db 574 GCGGGGCACTGTGCTGGAAGCGTAGACAGAGATGCAAGTATGTGTAGTGGATCG 633
QY 368 AGGATTGATCGTGGCTTAAGTGAAGACACGCTGCTGATGATGACAGCAGTGGCG 427
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QY 428 GCTGGGCGGACTTCAAGCTCTATACGGGAGCGGGCCCTGAGAGACGCAAGCGCTGTC 487
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Db 694 GCTGGGATCTTTGTGGAAGCTTATGGAACAATGACAGCAGCAGGAGCGGAAAGGCGC 753
QY 488 GGGAGGCAACTGGGCAATGAGTGAAGCAGAGTGTGACGGGGCGC 532
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Search completed: April 10, 2005, 20:17:22  
 Job time : 144.753 Secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 18:38:08 ; Search time 498.642 Seconds  
(without alignments)  
7060.905 Million cell updates/sec

Title: US-09-925-674B-8  
Perfect score: 581  
Sequence: 1 atgcccagcccccagcctcaac.....gcctttttgtcagcaagtg 581

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	563.4	97.0	582	9	US-09-925-674A-8 Sequence 8, Appl1
2	505.8	87.1	582	18	US-10-384-339C-37 Sequence 37, Appl1
3	505.8	87.1	583	9	US-09-925-674A-6 Sequence 6, Appl1
4	501	86.2	582	19	US-10-479-832A-4 Sequence 4, Appl1
5	364.4	62.7	1864	10	US-09-809-391-130 Sequence 130, App
6	364.4	62.7	1864	10	US-09-882-171-130 Sequence 130, App
7	364.4	62.7	1864	17	US-10-164-861-130 Sequence 130, App
8	364.2	62.7	578	16	US-10-029-386-10549 Sequence 10549, A
9	363.2	62.5	433	16	US-10-029-386-24249 Sequence 24249, A
10	212.2	36.5	6049	15	US-10-311-455-201 Sequence 201, App
11	191	32.9	6049	15	US-10-311-455-202 Sequence 202, App

12	140.4	24.2	660	17	US-10-402-017-9	Sequence 9, Appl1
13	139.6	24.0	540	17	US-10-402-017-5	Sequence 5, Appl1
14	139.4	24.0	600	17	US-10-402-017-7	Sequence 7, Appl1
15	138.8	23.9	151	16	US-10-029-386-27084	Sequence 27084, A
16	138.8	23.9	590	16	US-10-029-386-13384	Sequence 13384, A
17	137.8	23.7	150	9	US-09-864-761-17690	Sequence 17690, A
18	134.6	23.2	636	16	US-10-169-223-13	Sequence 13, Appl1
19	134.6	23.2	660	17	US-10-402-017-11	Sequence 11, Appl1
20	134.6	23.2	702	17	US-09-959-987-9	Sequence 9, Appl1
21	134.6	23.2	863	17	US-10-402-017-3	Sequence 3, Appl1
22	134.6	23.2	926	9	US-09-734-846-1	Sequence 1, Appl1
23	134.6	23.2	926	9	US-09-734-847A-39	Sequence 39, Appl1
24	134.6	23.2	926	9	US-09-952-278-5	Sequence 5, Appl1
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26	134.6	23.2	926	16	US-10-302-262-1	Sequence 1, Appl1
27	134.6	23.2	926	17	US-10-402-017-1	Sequence 1, Appl1
28	134.6	23.2	926	17	US-10-641-643-1430	Sequence 1430, Ap
29	134.6	23.2	926	18	US-10-717-597-87	Sequence 87, Appl
30	134.6	23.2	926	18	US-10-776-827-106	Sequence 106, App
31	134.6	23.2	926	18	US-10-825-282-47	Sequence 47, Appl
32	134.6	23.2	926	19	US-10-479-832A-3	Sequence 3, Appl1
33	134.6	23.2	1236	18	US-10-792-517-1	Sequence 1, Appl1
34	130.6	22.5	1455	18	US-10-792-517-7	Sequence 7, Appl1
35	126.8	21.8	600	9	US-09-864-761-7360	Sequence 7360, Ap
36	126.6	21.8	720	17	US-10-148-953A-8	Sequence 8, Appl1
37	126.4	21.8	1466	18	US-10-283-975A-394	Sequence 394, App
38	125.8	21.7	492	10	US-09-918-995-33305	Sequence 33305, A
39	125.8	21.7	555	9	US-09-864-761-24081	Sequence 24081, A
40	125.8	21.7	564	16	US-10-029-386-20790	Sequence 20790, A
41	125	21.5	717	16	US-10-053-645A-20	Sequence 20, Appl1
42	125	21.5	720	17	US-10-148-953A-6	Sequence 6, Appl1
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45	125	21.5	720	18	US-10-770-668-17	Sequence 17, Appl1

ALIGNMENTS

RESULT 1  
US-09-925-674A-8  
; Sequence 8, Application US/09925674A  
; Patent No. US20020119943A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES  
; FILE REFERENCE: 11686a  
; CURRENT APPLICATION NUMBER: US/09/925,674A  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/925,674  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: PN8965  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 582  
; TYPE: DNA  
; ORGANISM: Mouse  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(579)  
US-09-925-674A-8

Query Match 97.0%; Score 563.4; DB 9; Length 582;  
Best Local Similarity 98.1%; Pred. No. 2.9e-160;  
Matches 570; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGCCGACCCAGCCTCAACCCGACACACGCGCTAGTGGCTGACTTGTAGGCTAT 60  
Db 1 ATGCCGACCCAGCCTCAACCCGACACACGCGCTAGTGGCTGACTTGTAGGCTAT 60

QY 61 AGCTGAGCAGAGGGTTATGTCTGTGAGCTGGCCTGGGGAAGCCGCGCGAC 120  
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RESULT 2

US-10-384-339C-37  
 ; Sequence 37, Application US/10384339C  
 ; Publication No. US20040175703A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kreutzer, Roland  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GE  
 ; FILE REFERENCE: 20200/2002  
 ; CURRENT APPLICATION NUMBER: US/10/384,339C  
 ; PRIORITY FILING DATE: 2003-03-07  
 ; PRIOR APPLICATION NUMBER: PCT/EP02/00152  
 ; PRIORITY FILING DATE: 2002-01-09  
 ; PRIOR APPLICATION NUMBER: DE 10100586.5  
 ; PRIORITY FILING DATE: 2001-01-09  
 ; PRIOR APPLICATION NUMBER: DE 10155280.7  
 ; PRIORITY FILING DATE: 2001-10-26  
 ; PRIOR APPLICATION NUMBER: DE 10158411.3  
 ; PRIORITY FILING DATE: 2001-11-29  
 ; PRIOR APPLICATION NUMBER: DE 10160151.4  
 ; PRIORITY FILING DATE: 2001-12-07  
 ; NUMBER OF SEQ ID NOS: 173  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 37  
 ; LENGTH: 582  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; PUBLICATION INFORMATION:  
 ; TITLE: bcl-w  
 ; PATENT DOCUMENT NUMBER: US9747  
 ; US-10-384-339C-37

Query Match 87.1%; Score 505.8; DB 18; Length 582;  
 Best Local Similarity 91.9%; Pred. No. 7.8e-143;  
 Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 ATGCCGACCCAGCCTCAACCCCAAGACACACGCGCTCTAGTGCTGACTTTGTAGGCTAT 60

Db 1 ATGCCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGTTAT 60  
 QY 61 AGCTGAGCAGAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGCCGCGCGAC 120  
 |||  
 Db 61 AGCTGAGCAGAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGCCGCGCGAC 120  
 QY 121 CCGCTGACCAAGCCATGCGGGCTGTGAGACGAGTTTGAGACCCTTCCGCCGAC 180  
 |||  
 Db 121 CCGCTGACCAAGCCATGCGGGCTGTGAGACGAGTTTGAGACCCTTCCGCCGAC 180  
 QY 181 TTCTTGACCTGGCGCTCAGCTACACGTGACCCCAAGGCTCAGCCCAAGCAAGCTTCA 240  
 |||  
 Db 181 TTCTTGACCTGGCGCTCAGCTACACGTGACCCCAAGGCTCAGCCCAAGCAAGCTTCA 240  
 QY 241 CAGGTTCCGACGAATTTTCCAAAGGGGCGCTTAACTGGGCGCTTGTGGCATTTCTT 300  
 |||  
 Db 241 CAGGTTCCGACGAATTTTCCAAAGGGGCGCTTAACTGGGCGCTTGTGGCATTTCTT 300  
 QY 301 GTCTTTGGGCTGCCCTGTGTGCTGAGAGTGTCAAAAGAAATGAGCCCTTGTGGGA 360  
 |||  
 Db 301 GTCTTTGGGCTGCCCTGTGTGCTGAGAGTGTCAAAAGAAATGAGCCCTTGTGGGA 360  
 QY 361 CAAGTCCAGATTTGATCGTGGCCTACCTGAGACACGCTGCTGACTGATCCACAGC 420  
 |||  
 Db 361 CAAGTCCAGATTTGATCGTGGCCTACCTGAGACACGCTGCTGACTGATCCACAGC 420  
 QY 421 AGTGGCGGCTGGCGGACTTCACAGCTCTATACGGGGAAGGGCCCTGAGAGACGACGG 480  
 |||  
 Db 421 AGTGGCGGCTGGCGGACTTCACAGCTCTATACGGGGAAGGGCCCTGAGAGACGACGG 480  
 QY 481 CGTCTGCGGAGGGAAGTGGGCTGAGTGAAGCAGAGTGTGACGGGGCCGTGGCACTG 540  
 |||  
 Db 481 CGTCTGCGGAGGGAAGTGGGCTGAGTGAAGCAGAGTGTGACGGGGCCGTGGCACTG 540  
 QY 541 GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAGTG 581  
 |||  
 Db 541 GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAGTG 581

RESULT 3

US-09-925-674A-6  
 ; Sequence 6, Application US/09925674A  
 ; Patent No. US20020119943A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: AMRAD Operations Pty Ltd  
 ; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
 ; FILE REFERENCE: 11686a  
 ; CURRENT APPLICATION NUMBER: US/09/925,674A  
 ; PRIORITY FILING DATE: 2001-08-09  
 ; PRIOR APPLICATION NUMBER: 09/925,674  
 ; PRIORITY FILING DATE: 2001-08-09  
 ; PRIOR APPLICATION NUMBER: PN8965  
 ; PRIORITY FILING DATE: 1996-03-27  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 583  
 ; TYPE: DNA  
 ; ORGANISM: HUMAN  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1) .. (579)  
 ; US-09-925-674A-6

Query Match 87.1%; Score 505.8; DB 9; Length 583;  
 Best Local Similarity 91.9%; Pred. No. 7.8e-143;  
 Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 ATGCCGACCCAGCCTCAACCCCAAGACACACGCGCTCTAGTGCTGACTTTGTAGGCTAT 60  
 |||  
 Db 1 ATGCCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGTTAT 60



QY	61	AGCGTAGGCGAGAAAGGGTTATGTCTGTGAGACTGGGCTGGGGAAAGGCCAGCCGCCGAC	120
Db	61	AAGCTAGAGCAGAAAGGGTTATGTCTGTGAGACTGGCCCCGGGAGAGGCCAGACTGAC	120
QY	121	CCGCTGACCAAGCCATGCGGCTGCTGAGACGAGTTTGAGACCCGTTTCCGCCGACCC	180
Db	121	CCGCTGACCAAGCCATGCGGCGAGCTGAGATGAGTTCCAGACCCCGCTCCGGCGCAC	180
QY	181	TTCTCTGACCTGCGCCGCTCAGCTACACGTGACCCAGGCTCAGCCCAACGCTTCACC	240
Db	181	TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCCAACGCTTCACC	240
QY	241	CAGGTTTCCGACGAACCTTTTCCAAGGGGGCCCTAACTGGGGCCGCTTGTGSCATTCTT	300
Db	241	CAGGTTTCCGACGAACCTTTTCCAAGGGGGCCCAACTGGGGCCGCTTGTAGCCTTCTT	300
QY	301	GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAATGAGCCTTTGTGGGA	360
Db	301	GTCTTTGGGGCTGCACGTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA	360
QY	361	CAAGTCCAGGATTGGATCGTGSCCTTACTGTGAGACAACGCTGTGGCTGACTGCATCCACAGC	420
Db	361	CAAGTCCAGGAGTGGATGTGTGCTTACTGTGAGACGCGGCTGTGACTGATCCACAGC	420
QY	421	AGTGCGGGCTGGCGGACTTTCACAGCTCTATACGGGGACGGGGCCCTGAGAGACGCAACGG	480
Db	421	AGTGCGGGCTGGCGGAGTTTCACAGCTCTATACGGGGACGGGGCCCTGAGAGAGCGCGG	480
QY	481	CGTCTGCCGGAGGGCAACTGGGCATGAGTGAGACAAGTGSTGACGGGGCCGTGGCACTG	540
Db	481	CGTCTGCCGGAGGGGAACCTGGGCATCAGTGAGAGACAAGTGCTGACGGGGGCCGTGGCACTG	540
QY	541	GGGGCCCTGGTAACTGTAGGGGGCCTTTGTGCTAGCAAGTG	581
Db	541	GGGGCCCTGGTAACTGTAGGGGGCCTTTGTGCTAGCAAGTG	581

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RESULT 4
US-10-479-832A-4
; Sequence 4, Application US/10479832A
; Publication No. US20050064407A1
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson Research Pty Ltd
; TITLE OF INVENTION: bcl-2 DNazymes
; FILE REFERENCE: WJP13107942
; CURRENT APPLICATION NUMBER: US/10/479,832A
; CURRENT FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-479-832A-4

Query Match      86.2%; Score 501; DB 19; Length 582;
Best Local Similarity 91.4%; Pred. No. 2.2e-141;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY      1 ATGCCGACCCCGAGCCTCAACCCCGACACACAGCGGCTCTAGTGGCTGAATTGTAGGCTAT 60
       |||
Db      1 ATGGCGACCCCGAGCCTCGGGCCCCGACACACAGGGCTCTGGTGCGACTTTGTAGGTTAT 60

QY      61 AGCGTGAGGCAGAAAGGGTTATGTCTGTGGAGCTGGGGCTGGGGAGAAGGCCCGACCGCGAC 120
       |||
Db      61 AAGCTGAGGCAGAAAGGGTTATGTCTGTGGAGCTGGCCCCCGGGAGGGCCCCAGCAGCTGAC 120

QY      121 CCGCTGCACCACAAGCCCATATGCGGGCTGTGGAGACGAGTTTGAGACCCGTTTCGGCGCACCC 180
       |||
Db      121 CCGCTGCACCACAAGCCCATATGCGGGCTGTGGAGATGAGTTGAGACCCGCTTCGGCGCACCC 180

QY      181 TTCTCTGACCTGGCCGCTCAGCTAACGTGACCCCGAGGCTCAGGCGGACCGCAACGCTTACCC 240

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Db 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCCAACAGCTTCACC 240

QY 241 CAGGTTTCCGACGAACTTTCCAAAGGGGGCCCTAACTGGGGCCGTCTTGCGCATTTCTT 300

Db 241 CAGGTTTCCGATGAACTTTTCAAAGGGGGCCCAACTGGGGCCGCTTGTAGCTTCTT 300

QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGAGCCTTTGGTGGGA 360

Db 301 GTCTTTGGGGCTGCACGTGTGTGAGAGTGTCAACAAGAGATGAAACCACTGGTGGGA 360

QY 361 CAAGTCCAGGATTYGATCGTGGCCTACCTGGAGACACGTCGTGGCTGACTGGATCCACAGC 420

Db 361 CAAGTCCAGGATGATGTGTGGCTTACCTGGAGACGACGCTGGCTGACTGGATCCACAGC 420

QY 421 AGTGGCGGCTGGGCGGACTTCAAGCTCTATACGGGGACGGGGCCCTGGAGGACGCCACGG 480

Db 421 AGTGGGGGCTGGGCGGAGTTCAAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

QY 481 CGTCTGCGGGAGGCAACTGGGCATGAGTGAGCACAGTGTGACGGGGCCGTGGCACTG 540

Db 481 CGTCTGCGGGAGGGGAACGTGGGCATCAGTGAGGACAGTGTGACGGGGCCGTGGCACTG 540

QY 541 GGGGCCCTGTAACTGTAGGGGCCCTTTTGTCTAGCAAGTG 581

Db 541 GGGGCCCTGTAACTGTAGGGGCCCTTTTGTCTAGCAAGTG 581

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RESULT 5
US-09-809-391-130
; Sequence 130, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1648)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-809-391-130

Query Match          62.7%; Score 364.4; DB 10; length 1864;
Best Local Similarity 90.0%; Pred. No. 5.4e-100;
Matches 389; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

QY      1 ATGCCGACCCCAAGCCTCAACCCAGACACACCGCGCTAGTGCGTGAAGCTAT 60
      |||
Db      11 ATGGCGACCCCAAGCCTCGGCCCCAGACACACCGGCTCTGTGCGAGACTTGTAGGTTAT 70
      |||

QY      61 AGCGTAGGCAGAGGGTTATGTCTGTGAGCTGGGCTGGGGGAAGGCCAGCCGCGGAC 120
      |||
Db      71 AAGCTGAGGCAGAGGGTTATGTCTGTGAGCTGGCCCGGGGAGGGCCAGCAGCTGAC 130
      |||

QY      121 CCGCTGACCAAGCCATGCGGGCTGCTGAGAGCAGATTGAGACCCGTTCCGCGGAC 180
      |||
Db      131 CCGCTGACCAAGCCATGCGGGCAGCKGAGATGATTCAGAACCCGCTTCGCGGAC 190
      |||

QY      181 TTCTCTGACCTGGCGGCTCAGCTACACGTGACCCAGGCTCAGCCAGCAACGCTTAC 240
      |||
Db      191 TTCTCTGATCTGGCGGCTCAGCTGACATGTGACCCAGGCTCAGCCAGCAACGCTTAC 250
      |||

QY      241 CAGGTTCCGACGAAGCTTTTCCAAGGGGGCCCTAAGTGGGGCCGCTTGTGTGCAATCTTT 300
      |||

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Db 251 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCCTTCTT 310  
QY 301 GTCTTTGGGGCTGCCCTGTGTGTGAGAGTGTCAACAAGAAATGAGCCCTTGTGGGA 360  
Db 311 GTCTTTGGGGCTGCACTGTGTGTGAGAGTGTCAACAAGAGATGGAACCACTGTGGGA 370  
QY 361 CAAGTCCAGGATGATCGTGGCCTACTGAGACACACGCTGTGCTGACTGATCCACAGC 420  
Db 371 CAAGTGCAGAGATGATGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 430  
QY 421 AGTGGCGGCTGG 432  
Db 431 AGTGGGGGCTGG 442

## RESULT 6

US-09-882-171-130

/ Sequence 130, Application US/09882171  
/ Publication No. US20030175858A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Ruben et al.  
/ TITLE OF INVENTION: 186 Human Secreted proteins  
/ FILE REFERENCE: PZ002P2  
/ CURRENT APPLICATION NUMBER: US/09/882,171  
/ PRIOR FILING DATE: 2001-06-18  
/ PRIOR APPLICATION NUMBER: 09/809,391  
/ PRIOR FILING DATE: 2001-03-16  
/ PRIOR APPLICATION NUMBER: 09/149,476  
/ PRIOR FILING DATE: 1998-09-08  
/ PRIOR APPLICATION NUMBER: PCT/US98/04493  
/ PRIOR FILING DATE: 1998-03-06  
/ PRIOR APPLICATION NUMBER: 60/040,162  
/ PRIOR FILING DATE: 1997-03-07  
/ PRIOR APPLICATION NUMBER: 60/040,333  
/ PRIOR FILING DATE: 1997-03-07  
/ PRIOR APPLICATION NUMBER: 60/038,621  
/ PRIOR FILING DATE: 1997-03-07  
/ PRIOR APPLICATION NUMBER: 60/040,626  
/ PRIOR FILING DATE: 1997-03-07  
/ PRIOR APPLICATION NUMBER: 60/040,334  
/ PRIOR FILING DATE: 1997-03-07  
/ PRIOR APPLICATION NUMBER: 60/040,336  
/ PRIOR FILING DATE: 1997-03-07  
/ PRIOR APPLICATION NUMBER: 60/040,163  
/ PRIOR FILING DATE: 1997-03-07  
/ PRIOR APPLICATION NUMBER: 60/047,600  
/ PRIOR FILING DATE: 1997-05-23  
/ PRIOR APPLICATION NUMBER: 60/047,615  
/ PRIOR FILING DATE: 1997-05-23  
/ PRIOR APPLICATION NUMBER: 60/047,597  
/ PRIOR FILING DATE: 1997-05-23  
/ PRIOR APPLICATION NUMBER: 60/047,502  
/ PRIOR FILING DATE: 1997-05-23  
/ PRIOR APPLICATION NUMBER: 60/047,633  
/ PRIOR FILING DATE: 1997-05-23  
/ PRIOR APPLICATION NUMBER: 60/047,583  
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/ PRIOR APPLICATION NUMBER: 60/047,617  
/ PRIOR FILING DATE: 1997-05-23  
/ PRIOR APPLICATION NUMBER: 60/047,618  
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/ PRIOR APPLICATION NUMBER: 60/047,584  
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/ PRIOR FILING DATE: 1997-05-23

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/ PRIOR FILING DATE: 1997-05-23  
/ PRIOR APPLICATION NUMBER: 60/047,598  
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/ PRIOR APPLICATION NUMBER: 60/047,613  
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/ PRIOR FILING DATE: 1997-05-23  
/ PRIOR APPLICATION NUMBER: 60/047,601  
/ PRIOR FILING DATE: 1997-05-23  
/ PRIOR APPLICATION NUMBER: 60/043,580  
/ PRIOR FILING DATE: 1997-04-11  
/ PRIOR APPLICATION NUMBER: 60/043,568  
/ PRIOR FILING DATE: 1997-04-11  
/ PRIOR APPLICATION NUMBER: 60/043,314  
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/ PRIOR APPLICATION NUMBER: 60/043,569  
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/ PRIOR FILING DATE: 1997-04-11  
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/ PRIOR APPLICATION NUMBER: 60/043,313  
/ PRIOR FILING DATE: 1997-04-11  
/ PRIOR APPLICATION NUMBER: 60/043,672  
/ PRIOR FILING DATE: 1997-04-11  
/ PRIOR APPLICATION NUMBER: 60/043,315  
/ PRIOR FILING DATE: 1997-04-11  
/ PRIOR APPLICATION NUMBER: 60/048,974  
/ PRIOR FILING DATE: 1997-06-06  
/ PRIOR APPLICATION NUMBER: 60/056,886  
/ PRIOR FILING DATE: 1997-08-22  
/ PRIOR APPLICATION NUMBER: 60/056,877  
/ PRIOR FILING DATE: 1997-08-22  
/ PRIOR APPLICATION NUMBER: 60/056,889  
/ PRIOR FILING DATE: 1997-08-22  
/ PRIOR APPLICATION NUMBER: 60/056,893  
/ PRIOR FILING DATE: 1997-08-22  
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/ PRIOR FILING DATE: 1997-08-22  
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/ PRIOR APPLICATION NUMBER: 60/056,637  
/ PRIOR FILING DATE: 1997-08-22  
/ PRIOR APPLICATION NUMBER: 60/056,903  
/ PRIOR FILING DATE: 1997-08-22  
/ PRIOR APPLICATION NUMBER: 60/056,888  
/ PRIOR FILING DATE: 1997-08-22  
/ PRIOR APPLICATION NUMBER: 60/056,879  
/ PRIOR FILING DATE: 1997-08-22  
/ PRIOR APPLICATION NUMBER: 60/056,880  
/ PRIOR FILING DATE: 1997-08-22  
/ PRIOR APPLICATION NUMBER: 60/056,894  
/ PRIOR FILING DATE: 1997-08-22  
/ PRIOR APPLICATION NUMBER: 60/056,911

PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/056,636  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/056,874  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/056,910  
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PRIOR APPLICATION NUMBER: 60/056,864  
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PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/056,845  
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PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/056,909  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/056,875  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/056,862  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/056,887  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/056,908  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/048,964  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/057,650  
PRIOR FILING DATE: 1997-09-05  
PRIOR APPLICATION NUMBER: 60/056,884  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/057,669  
PRIOR FILING DATE: 1997-09-05

Query Match 62.7%; Score 364.4; DB 10; Length 1864;

Best Local Similarity 90.0%; Pred. No. 5.4e-100;  
Matches 389; Conservative 1; Mismatches 42; Indels 0; Gaps 0;  
QY 1 ATGCCGACCCAGCCTCAACCCAGACACGCGCTTAGTGCTGACTTTGTAGGCTAT 60  
DB 11 ATGGCAGCCAGCCTCGGCCAGACACGCGCTCTGTGGCAGACTTTGTAGGTTAT 70  
QY 61 AGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGGCTGGGAAGGCCAGCCGCGAC 120  
DB 71 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGCCCGGAGAGGCCAGACTGAC 130  
QY 121 CCGCTGACCAAGCCATGCGGGCTGTGAGAGAGATTGAGACCCGTTCCGCGCAC 180  
DB 131 CCGCTGACCAAGCCATGCGGGCAGCKGAGATGAGTTCGAGACCGGCTTCGCGCAC 190  
QY 181 TTCTGTAGCTGCGCGCTCAGCTACAGTACACCCAGGCTCAGCCAGCAAGCTTACC 240  
DB 191 TTCTGTAGCTGCGCGCTCAGCTCAGTATGACCCAGGCTCAGCCAGCAAGCTTACC 250  
QY 241 CAGGTTCCGACGAACCTTTCCAGAGGGGCGCTTAAGTGGGCGCTTGTGCAATCTTT 300  
DB 251 CAGGTTCCGACGAACCTTTCCAGAGGGGCGCTTAAGTGGGCGCTTGTGCAATCTTT 310  
QY 301 GTCTTTGGGCTGCCCTGTGTGCTGAGAGTCAACAAAGAAATGAGCTTTGTGGA 360  
DB 311 GTCTTTGGGCTGCACTGTGTGCTGAGAGTCAACAAAGAGATGAACTGTGGA 370  
QY 361 CAAGTCAGAGATTGATGATGAGCTGAGCTTGAAGACAGCTGTGCTGATCCAGC 420  
DB 371 CAAGTCAGAGATTGATGATGAGCTTGAAGACAGCTGTGCTGATCCAGC 430  
QY 421 AGTGGCGGCTGG 432  
DB 431 AGTGGCGGCTGG 442

RESULT 7  
US-10-164-861-130  
; Sequence 130, Application US/10164861  
; Publication No. US20030225248A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR FILING DATE: US/09/149,476  
; PRIOR APPLICATION NUMBER: US/09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 757  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 130  
; LENGTH: 1864  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1648)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-10-164-861-130

Query Match 62.7%; Score 364.4; DB 17; Length 1864;  
Best Local Similarity 90.0%; Pred. No. 5.4e-100;  
Matches 389; Conservative 1; Mismatches 42; Indels 0; Gaps 0;  
QY 1 ATGCCGACCCAGCCTCAACCCAGACACGCGCTTAGTGCTGACTTTGTAGGCTAT 60  
DB 11 ATGGCAGCCAGCCTCGGCCAGACACGCGCTCTGTGGCAGACTTTGTAGGTTAT 70  
QY 61 AGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGGCTGGGAAGGCCAGCCGCGAC 120  
DB 71 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGCCCGGAGAGGCCAGACTGAC 130

QY 121 CCGCTGACCAAGCCATGCGGGCTGCTGAGACGAGTTTGAACCCGTTCCCGCCGACC 180  
DB 131 CCGCTGACCAAGCCATGCGGGCTGCTGAGACGAGTTTGAACCCGTTCCCGCCGACC 180  
QY 181 TTCTTGACCTGGCGCTGCTGAGACGAGTTTGAACCCGTTCCCGCCGACC 180  
DB 191 TTCTTGACCTGGCGCTGCTGAGACGAGTTTGAACCCGTTCCCGCCGACC 180  
QY 241 CAGGTTCCGACGAATTTTCCAGAGGGGCGCTTACTGGGCGCTTGTGCAATTCTT 250  
DB 251 CAGGTTCCGACGAATTTTCCAGAGGGGCGCTTACTGGGCGCTTGTGCAATTCTT 250  
QY 301 GTCTTTGGGGCTGCGCTGCTGAGAGTGTCAACAAGAAATGAGCCCTTGTGCAATTCTT 300  
DB 311 GTCTTTGGGGCTGCGCTGCTGAGAGTGTCAACAAGAAATGAGCCCTTGTGCAATTCTT 300  
QY 361 CAGTCCAGAGTTGATGCTGGCTTACTGAGAGACAGTCTGCTGATGATCCAGC 420  
DB 371 CAGTCCAGAGTTGATGCTGGCTTACTGAGAGACAGTCTGCTGATGATCCAGC 420  
QY 421 AGTGGCGCTGG 432  
DB 431 AGTGGCGCTGG 442

RESULT 8  
US-10-029-386-10549  
; Sequence 10549, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 10549  
; LENGTH: 578  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR14.3  
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 4.2  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.3  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.2  
; OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUE 0.00e+00  
; OTHER INFORMATION: NT HIT: g114751151, EVALUE 0.00e+00  
; US-10-029-386-10549  
; SWISSPROT HIT: Q92843, EVALUE 2.00e-72

Query Match  
Best Local Similarity 62.7%; Score 364.2; DB 16; Length 578;  
Matches 390; Conservative 0; Mismatches 43; Indels 0; Gaps 0;  
DB 1 ATGCCGACCCCAAGCTTCAACCCAGACACACCGCTCTAGTGGCTGATTTGTAGGCTAT 60  
QY 105 ATGCCGACCCCAAGCTTCAACCCAGACACACCGCTCTAGTGGCTGATTTGTAGGCTAT 60  
DB 61 AGCTGAGGAGAGGTTATGTTGAGAGTGGGCTGAGAGAGGCGCCGAGCCGCGAC 120  
QY 165 AAGCTGAGGAGAGGTTATGTTGAGAGTGGGCTGAGAGAGGCGCCGAGCCGCGAC 120  
DB 121 CCGCTGACCAAGCCATGCGGGCTGCTGAGACGAGTTTGAACCCGTTCCCGCCGACC 180  
QY 225 CCGCTGACCAAGCCATGCGGGCTGCTGAGACGAGTTTGAACCCGTTCCCGCCGACC 180

QY 181 TTCTTGACCTGGCGCTGCTGAGACGAGTTTGAACCCGTTCCCGCCGACC 180  
DB 285 TTCTTGACCTGGCGCTGCTGAGACGAGTTTGAACCCGTTCCCGCCGACC 180  
QY 241 CAGGTTCCGACGAATTTTCCAGAGGGGCGCTTACTGGGCGCTTGTGCAATTCTT 250  
DB 345 CAGGTTCCGACGAATTTTCCAGAGGGGCGCTTACTGGGCGCTTGTGCAATTCTT 250  
QY 301 GTCTTTGGGGCTGCGCTGCTGAGAGTGTCAACAAGAAATGAGCCCTTGTGCAATTCTT 300  
DB 405 GTCTTTGGGGCTGCGCTGCTGAGAGTGTCAACAAGAAATGAGCCCTTGTGCAATTCTT 300  
QY 361 CAGTCCAGAGTTGATGCTGGCTTACTGAGAGACAGTCTGCTGATGATCCAGC 420  
DB 465 CAGTCCAGAGTTGATGCTGGCTTACTGAGAGACAGTCTGCTGATGATCCAGC 420  
QY 421 AGTGGCGCTGG 433  
DB 525 AGTGGCGCTGG 537

RESULT 9  
US-10-029-386-24249  
; Sequence 24249, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 24249  
; LENGTH: 433  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR14.3  
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 4.2  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.3  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.2  
; OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUE 0.00e+00  
; OTHER INFORMATION: NT HIT: g114751151, EVALUE 0.00e+00  
; US-10-029-386-24249  
; SWISSPROT HIT: Q92843, EVALUE 2.00e-72

Query Match  
Best Local Similarity 62.5%; Score 363.2; DB 16; Length 433;  
Matches 389; Conservative 0; Mismatches 43; Indels 0; Gaps 0;  
DB 1 ATGCCGACCCCAAGCTTCAACCCAGACACACCGCTCTAGTGGCTGATTTGTAGGCTAT 60  
QY 2 ATGCCGACCCCAAGCTTCAACCCAGACACACCGCTCTAGTGGCTGATTTGTAGGCTAT 60  
DB 61 AGCTGAGGAGAGGTTATGTTGAGAGTGGGCTGAGAGAGGCGCCGAGCCGCGAC 120  
QY 62 AAGCTGAGGAGAGGTTATGTTGAGAGTGGGCTGAGAGAGGCGCCGAGCCGCGAC 120  
DB 121 CCGCTGACCAAGCCATGCGGGCTGCTGAGACGAGTTTGAACCCGTTCCCGCCGACC 180  
QY 181 TTCTTGACCTGGCGCTGCTGAGACGAGTTTGAACCCGTTCCCGCCGACC 180  
DB 182 TTCTTGACCTGGCGCTGCTGAGACGAGTTTGAACCCGTTCCCGCCGACC 180



OY 241 CAGTTTCCGACGAACCTTTTCCAAAGGGGCCCTTAACCTGGGCCGCTTGTGGCATTTCTTT 300  
DB 242 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCCTTCTTT 301  
OY 301 GTCTTTGGGGCTGCCCTGTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCTTTGTGGGA 360  
DB 302 GTCTTTGGGGCTGCACTGTGTGTGTGAGAGTGTCAACAAAGAGATGAACCACTGTGGGA 361  
OY 361 CAAGTCCAGATTGATCGTGGCCTACCTGAGACACGCTGTGCTGACTGTGATCCACAGC 420  
DB 362 CAAGTCCAGAGTGAATGTGTGGCCTACCTGAGACGACGCTGCTGACTGTGATCCACAGC 421  
OY 421 AGTGGCGGCTGG 432  
DB 422 AGTGGGGGCTGG 433

RESULT 10

US-10-311-455-201  
; Sequence 201, Application US/10311455  
; Publication No. US20030143606A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ  
; TITLE OF INVENTION: cytosine methylation  
; FILE REFERENCE: 5013.1014  
; CURRENT APPLICATION NUMBER: US/10/311,455  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: PCT/EP01/07537  
; PRIOR FILING DATE: 2001-07-02  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 2424  
; SEQ ID NO 201  
; LENGTH: 6049  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-311-455-201

Query Match 36.5%; Score 212.2; DB 15; Length 6049;  
Best Local Similarity 68.1%; Pred. No. 7e-54;  
Matches 295; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

OY 1 ATGCCGACCCCAAGCTTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGAGGCTAT 60  
DB 5001 ATGGCGATTTTAGTTTCGGTTTATAGATATACGGGTTTGGTGTAGATTGTTAGGTTAT 5060  
OY 61 AGGCTGAGGCAAGGGTTATGTCTGTGAGCTGGGCTGGGAAGGCCAGCCGCGGAC 120  
DB 5061 AAGTTGAGGTAGAAGGGTTATGTCTGTGAGCTGGGCTGGGAAGGGTTAGATTGAT 5120  
OY 121 CCGCTGACCAAGCCATGCGGGCTGTGAGACGAGTTTGAGACCCGTTCCGCGGAC 180  
DB 5121 TCGTTGATTAAGTTATGCGGGTAGTTGAGATGAGTTGAGATTCCGTTCCGCGTATT 5180  
OY 181 TTCTGTGACCTGGCCGCTCAGCTACACGTCAGCCCAAGGCTCAGCCCAAGCAGCTTACC 240  
DB 5181 TTTTGTGATTTGGCGGTTTGTGTATGATTTAGGTTTAAATTAAATGATTAAGTTTATT 5240  
OY 241 CAGTTTCCGACGAACCTTTTCCAAAGGGGCCCTTAACCTGGGCCGCTTGTGGCATTTCTTT 300  
DB 5241 TAGTTTTCGATGAATTTTAAAGGGGTTTAAATGGGGTGTGTTTGTAGTTTCTTTT 5300  
OY 301 GTCTTTGGGGCTGCCCTGTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCTTTGTGGGA 360  
DB 5301 GTTTTGGGGTGTGATTTGTGTGTGAGAGTGTAAATGAAGATGAATTAATTTGTGGGA 5360

OY 361 CAAGTCCAGATTGATCGTGGCCTAAGAGACACAGCTGTGCTGACTGTGATCCACAGC 420  
DB 5361 TAAGTGTAGAGATGATGTGTGTTTATTTGAGACGTAAGTTGGTTGATTTAGT 5420  
OY 421 AGTGGCGGCTGGG 433  
DB 5421 AGTGGGGGTTGGG 5433

RESULT 11

US-10-311-455-202/c  
; Sequence 202, Application US/10311455  
; Publication No. US20030143606A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ  
; TITLE OF INVENTION: cytosine methylation  
; FILE REFERENCE: 5013.1014  
; CURRENT APPLICATION NUMBER: US/10/311,455  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: PCT/EP01/07537  
; PRIOR FILING DATE: 2001-07-02  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 2424  
; SEQ ID NO 202  
; LENGTH: 6049  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-311-455-202

Query Match 32.9%; Score 191; DB 15; Length 6049;  
Best Local Similarity 65.7%; Pred. No. 1.8e-47;  
Matches 278; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

OY 1 ATGCCGACCCCAAGCTTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGAGGCTAT 60  
DB 1049 ATACGACCCCAAGCTTCAACCCAGACACACGAACTTAATTAACAATTATTAATAT 990  
OY 61 AGGCTGAGGCAAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGCCGCGGAC 120  
DB 989 AAACATAAACAATAAATAATATATCTAATAAATAAACCCGAAATAAATAAACCACTAAC 930  
OY 121 CCGCTGACCAAGCCATGCGGGCTGTGAGACGAGTTTGAGACCCGTTCCGCGGAC 180  
DB 929 CCGTACACCAAAACCATACGAACTAATAAATAATTCGAAACCGCTTCCGAGCGACC 870  
OY 181 TTCTGTGACCTGGCCGCTCAGCTACAGTGAACCCAGGCTCAGCCCAAGCAGCTTACC 240  
DB 869 TTCTGTATCTAAGACTCAACTACATATAACCCCAACTCAACCAACGCTTACC 810  
OY 241 CAGTTTCCGACGAACCTTTTCCAAAGGGGCCCTTAACCTGGGGCGCTTGTGGCATTTCTTT 300  
DB 809 CAATCTCCGATTAACCTTTTCAAAAAAACCCTTAATTAACCTTCTTT 750  
OY 301 GTCTTTGGGGCTGCCCTGTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCTTTGTGGGA 360  
DB 749 ATCTTAATACTACATATATCTAATAAATAATATCAACAAAAAATAAATAACCACTAATA 690  
OY 361 CAAGTCCAGATTGATCGTGGCCTAAGAGACACAGCTGTGCTGACTGTGATCCACAGC 420  
DB 689 CAATATCAAAATAAATAATTAACCTAATAAAGCAACTAATACTAATAATCCACAAAC 630  
OY 421 AGT 423  
DB 629 AAT 627

## RESULT 12

US-10-402-017-9  
; Sequence 9, Application US/10402017  
; Publication No. US20030219871A1  
; GENERAL INFORMATION:  
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGER  
; TITLE OF INVENTION: Host cells having improved survival properties and methods to gen  
; TITLE OF INVENTION: such cells  
; FILE REFERENCE: Case 1/1314  
; CURRENT APPLICATION NUMBER: US/10/402,017  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: US 60/369,307  
; PRIOR APPLICATION NUMBER: April 2, 2002  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 660  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:3 (del166-83)  
US-10-402-017-9

Query Match 24.2%; Score 140.4; DB 17; Length 660;  
Best Local Similarity 57.5%; Pred. No. 2.8e-32;  
Matches 252; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

QY 95 GGCCTGGGAAGGCCAGCCGCGACCCGCTGCAACCAAGCATGCGGCTGTGAGACG 154  
DB 185 GCCCCGCGTAGCGCGCGACAGCAGCCGTAAGCAAGCGCTGAGAGAGGCCGCGATG 244  
QY 155 AGTTGAGACCCGTTTCGCGCGACCTTCTGTGACCTGCGCGCTCAGCTACAGTGACCC 214  
DB 245 AGTTGAGCTGCGGTACCGCGCGCTTCACTGATCTAACATCCAGCTTCAATATACCC 304  
QY 215 CAGGCTCAGCCCAAGCAAGCTTCAACCAAGTTCCGACGAATTTCCAGGGGCCCTA 274  
DB 305 CAGGACTGCATATCAAGCTTTGAACAGGTGATGAATGAATCTTCCGGGATGGGTA 364  
QY 275 ACTGGGCGCGCTTGTGGCATTTCTTGTCTTTGGGGCTGCCGTGTGTGAGAGTCA 334  
DB 365 ACTGGGCTCGCATTTGTGGCTTTTCTCTCTTGGTGAGCCCTCTGTGTGAAAGCGTAG 424  
QY 335 ACAAGAATGAGCCTTTGTGGGACAAGTCCAGGATTGATCGTGCGCTACCTGAGGA 394  
DB 425 ACAAGAGATGAGGTATTGTGATGCGATCGCAAGTTGATGCGCACTTCACTGAATG 484  
QY 395 CACGTCTGCTGACTGATCCACAGCAGTGGCGGCTGGCGGACTTCAAGCTTATACG 454  
DB 485 ACCACCTAGAGCCTTGGATCCAGGACCAACGCGGCTGGGACACTTTCGTGAACCTACG 544  
QY 455 GGGACGGGCGCTGGAGAGCAGCAGCGCTGTGCGGAGGGCAACTGGGCAATGAGTGA 514  
DB 545 GAAACAATGACAGAGCTGAGAGCGGAAAGGCCAGGAGCGCTTCAACCGCTGTTCTGA 604  
QY 515 CAGTGTGACGGGGCGG 532  
DB 605 CGGGCATGACTGTGCTG 622

## RESULT 13

US-10-402-017-5  
; Sequence 5, Application US/10402017  
; Publication No. US20030219871A1  
; GENERAL INFORMATION:  
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGER  
; TITLE OF INVENTION: Host cells having improved survival properties and methods to gen  
; TITLE OF INVENTION: such cells  
; FILE REFERENCE: Case 1/1314  
; CURRENT APPLICATION NUMBER: US/10/402,017  
; CURRENT FILING DATE: 2003-03-28

; PRIOR APPLICATION NUMBER: US 60/369,307  
; PRIOR APPLICATION NUMBER: April 2, 2002  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 540  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:3 (del126-83)  
US-10-402-017-5

Query Match 24.0%; Score 139.6; DB 17; Length 540;  
Best Local Similarity 56.7%; Pred. No. 4.8e-32;  
Matches 287; Conservative 0; Mismatches 204; Indels 15; Gaps 1;

QY 27 CACACGCGCTTAGTGGCTGACTTTGTAGCTATAGGCTGAGGCAAGGTTATGCTG 86  
DB 12 CAACCGGAGCTAGTGTGACTTCTCTCTACAGCTCTCCAGAAAGATACAGCTG 71  
QY 87 TGAAGTGGGCTGGGAAGGCCAGCCGCGACCCGCTGCAACCAAGCATGCGGCTGC 146  
DB 72 GAGTGGCG-----CCGACAGCAGCAGCCGTAAGCAAGCGCTGAGAGAGGC 116  
QY 147 TGAAGAGAGTTTGAGACCCGTTCCGCGCACCTTCTGACCTGCGGCTCAGCTACA 206  
DB 117 CGGCGATGAGTTTGAGCTGCGGTACCGGCGGCGGCTCAGTATCTAACATCCAGCTTCA 176  
QY 207 CGTACCCCAAGGCTCAGCCCAAGCAAGCTTCAACCAAGTTTCCAGCAACTTTCCAGG 266  
DB 177 TATAACCCCAAGGACTGCATATCAAGCTTTGAACAGGTAGTGAATGAATCTTCCGGGA 236  
QY 267 GGGCCCTAAGTGGGCGCTTGTGGCATTTCTTGTCTTTGGGGCTGCCGTGTGTGTA 326  
DB 237 TGGGTAAACTGGGCTGCAATGTGGCTTTTCTCTCTGCTGAGAGCCCTGTGTGGA 296  
QY 327 GAGTCAACAAGAAATGAGCCTTGTGGGACAAGTCCAGGATTGATCGTGCGCTA 386  
DB 297 AAGCTAGACAAGAGATGAGGTATTGTGATGCGATCGCAAGTTGATGCGCACTTA 356  
QY 387 CCTGAGACACGTCTGCTGACTGATCCACAGCAGTGGCGGCTGGCGGACTTCAAGC 446  
DB 357 CCTGATGACCACTAGAGCCTTGGATCCAGGACCAACGCGGCTGGGACACTTTCGTGA 416  
QY 447 TCTATAGGGGAGCGGGCCCTGAGAGACGCAAGCGCTGTGCGGAGGGCAACTGGGATG 506  
DB 417 ACTCTAGGAACAATGACAGCAGTGAAGAGCCGAAAGGCCAGAGCGCTTCAACCGCTG 476  
QY 507 AGTGACACAGTGTGACGGGGCGG 532  
DB 477 GTTCTGACGGGCGATGACTGTGCTG 502

## RESULT 14

US-10-402-017-7  
; Sequence 7, Application US/10402017  
; Publication No. US20030219871A1  
; GENERAL INFORMATION:  
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGER  
; TITLE OF INVENTION: Host cells having improved survival properties and methods to gene  
; TITLE OF INVENTION: such cells  
; FILE REFERENCE: Case 1/1314  
; CURRENT APPLICATION NUMBER: US/10/402,017  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: US 60/369,307  
; PRIOR APPLICATION NUMBER: April 2, 2002  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 600  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

OTHER INFORMATION: Deletion mutant of SEQ ID NO:3 (del46-83)  
US-10-402-017-7

Query Match 24.0%; Score 139.4; DB 17; Length 600;  
Best Local Similarity 57.1%; Pred. No. 5.6e-32;  
Matches 254; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

QY 88 GGAGCTGGGCTGGGGAAGGCCAGCCCGGACCCGCTGCACCAAGCCATGGGGCTGCT 147  
DB 118 GGAAGTGAATCAGAGAGGGCGCGCCGACAGCAGCCGTAAGCAAGCGCTGAGAGAGGCC 177  
QY 148 GGAGACGAGTTTGAGACCCGTTTCCGCGCACCTTCTTGACCTGGCCGCTGACTACAC 207  
DB 178 GGCATGAGTTTGAGCTGCGGTACCGCGGCGTTCAATGATCTAACATCCAGCTTCAT 237  
QY 208 GTGACCCAGGCTCAGCCAGCAACGCTTACCCAGGTTTCCGACGAATTTCCAGAGG 267  
DB 238 ATAAACCCAGGAGCTGCATATCAAGCTTGAACAGTAGTGAATGAATCTTCCGGGAT 297  
QY 268 GGGCCTAAGTGGGCGCTTGTGCTGCTTGTGCTTGTGCTGCTGCTGCTGCTGCTGAG 327  
DB 298 GGGTAACTGGGGTCCGATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 357  
QY 328 AGTGTCAACAAAGAAATGAGCCCTTGTGGAACAATCCAGATTGATGCTGCTGCTAC 387  
DB 358 AGCGTAGACAGAGAGATGAGGTATTGTGATCGAATCGCAAGTTGATGAGCCACTAC 417  
QY 388 CTGAGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 447  
DB 418 CTGAATGACCACTAGACCTTGTGATCCAGACAAACGCGCTGGGACACTTTCGTGAA 477  
QY 448 CTATACGGGAGCGGGCCCTGAGAGACGACGCGCTTGCAGGAGGCACTGGGCATGA 507  
DB 478 CTCTACGGAACATGACAGCAGCTGAGAGCCGGAAGGCCAGAGCGCTTCAACCGCTGG 537  
QY 508 GTGAGCACAGTGTGACGGGGCGG 532  
DB 538 TTCCTGACGGGCACTGCTGCTG 562

RESULT 15

US-10-029-386-27084  
; Sequence 27084, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
; FILE REFERENCE: AEOICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 27084  
; LENGTH: 151  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR14.3  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2  
; OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUE 5.00e-70  
; OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 3.00e-11  
; OTHER INFORMATION: NT HIT: g114574571, EVALUE 9.00e-80  
US-10-029-386-27084

Query Match 23.9%; Score 138.8; DB 16; Length 151;  
Best Local Similarity 95.3%; Pred. No. 7.1e-32;  
Matches 143; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 432 GCGGACTTCAAGCTCTATACGGAGCGGGCCCTGAGAGACGACGCGGCTGCGGA 491

DB 1 GCGGAGTTCAAGCTCTATACGGGAGCGGGCCCTGAGAGAGCGCGGCTGCGGGA 60  
QY 492 GGGCACTGGGCACTGAGTACAGACAGTGTGACGGGGCCGCTGGCACTGGGGCCCTGTG 551  
DB 61 GGGGAAGTGGGCACTGAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120  
QY 552 AACTGTAGGGGCTTTTGTGCTAGCAAGTG 581  
DB 121 AACTGTAGGGGCTTTTGTGCTAGCAAGTG 150

Search completed: April 10, 2005, 22:38:34  
Job time : 500.642 secs

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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 14:47:25 ; Search time 2831.63 Seconds  
(without alignments)  
7810.120 Million cell updates/sec

Title: US-09-925-674B-8

Perfect score: 581

Sequence: 1 atgcgcagccagccctcaac.....gcctttttgtcagcaagtg 581

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_hic:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gss1:\*
- 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	560.2	96.4	582	AY421022	AY421022 Mus muscu
2	560.2	96.4	1949	AK015644	AK015644 Mus muscu
3	560.2	96.4	3487	AK004680	AK004680 Mus muscu
4	558.6	96.1	969	BY715200	BY715200 BY715200
5	503.6	86.7	967	BU503850	BU503850 AGENCOURT
6	501	86.2	582	AY421020	AY421020 Homo sapi
7	501	86.2	727	CD617893	CD617893 56057475J
8	499.4	86.0	629	CD617891	CD617891 56057367J
9	477.6	82.2	804	AL157542	AL157542 DKFZP761D
10	477	82.1	1030	BE793530	BE793530 601590016
11	471.2	81.1	713	BP753931	BP753931
12	456.6	78.6	757	CK359685	CK359685 AGENCOURT
13	456	78.5	643	7 CN281020	CN281020 170005318
14	447.8	77.1	662	6 CD617892	CD617892 56057475H
15	432.8	74.5	627	6 CD617890	CD617890 56057367H
16	429	73.8	815	2 BF785386	BF785386 602111728
17	421.8	72.6	854	3 AK013244	AK013244 Mus muscu
18	413	71.1	697	4 BI770566	BI770566 603060362
19	409	70.4	792	4 BG298789	BG298789 602396527
20	407.4	70.1	623	6 CB578463	CB578463 AMGNNUC:N
21	403.6	69.5	540	2 AW258810	AW258810 um74a02.Y
22	387.2	66.6	516	7 CN281015	CN281015 170005321
23	382.2	65.8	626	6 CA391923	CA391923 C820C09.Y
24	374	64.4	630	7 CO040065	CO040065 UI-M-BH1-

25	364.6	62.8	752	7	CO401477	CO401477 AGENCOURT
26	364	62.7	583	5	BP355256	BP355256 BP355256
27	362.2	62.3	583	5	BP249141	BP249141 BP249141
28	362.2	62.3	584	5	BP311709	BP311709 BP311709
29	359.4	61.9	583	5	BP202031	BP202031 BP202031
30	357.2	61.5	643	4	BI910270	BI910270 603069493
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ALIGNMENTS

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DEFINITION Mus musculus BCL2L2 gene, VIRUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY421022  
VERSION AY421022.1 GI:39776979  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE  
AUTHORS Clark,A.G., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.  
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Best Local Similarity 97.8%; Pred. No. 3.2e-134;  
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
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QY	541	GGGGCCCTGTAACTGTAGGGGCCCTTTTGTCTAGCAAGTG	581
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AK015644	AK015644	1949 bp mRNA linear HTC 03-APR-2004	AK015644	GI:12854052	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:493048D08 product:Bcl2-like 2, full insert sequence.	HTC; CAP trapper.	Mus musculus (house mouse)	1	Carninci, P. and Hayashizaki, Y.	High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)	99279253	10349636	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Genome Res. 10 (10), 1617-1630 (2000)	20499374	11042159	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.	

konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J.,

TITLE	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format
MEDLINE	sequencing pipeline with 384 multicapillary sequencer
PUBMED	Genome Res. 10 (11), 1757-1771 (2000)
REFERENCE	20530913
AUTHORS	11076861
TITLE	4
JOURNAL	The RIKEN Genome Exploration Research Group Phase II Team and the
REFERENCE	FANTOM Consortium.
AUTHORS	Functional annotation of a full-length mouse cDNA collection
TITLE	Nature 409, 685-690 (2001)
JOURNAL	5
REFERENCE	The FANTOM Consortium and the RIKEN Genome Exploration Research
AUTHORS	Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation
JOURNAL	of 60,770 full-length cDNAs
REFERENCE	Nature 420, 563-573 (2002)
AUTHORS	6 (bases 1 to 1949)
TITLE	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
JOURNAL	Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
REFERENCE	Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
AUTHORS	Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,
TITLE	Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,
JOURNAL	Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
REFERENCE	Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
AUTHORS	Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
TITLE	Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
JOURNAL	Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
REFERENCE	Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
AUTHORS	Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of

COMMENT Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAGAGAGCTCTTTTCTTTTCTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAATTAATTAATATCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLX I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

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Query Match      96.4%; Score 560.2; DB 3; Length 3487;
Best Local Similarity 97.8%; Pred. No. 4.3e-134;
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY      1 ATGCCGACCCCGCCTCAACCCGAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db      209 ATGGCGACCCCGCCTCAACCCGAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 268
QY      61 AGGCTGAGGCGAGAAAGGTTATGTCTGTGGAGCTGGGCTGGGGAAGGCCAGCCGCCGAC 120
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LOCUS   BY715200 969 bp mRNA linear EST 17-DEC-2002
DEFINITION BY715200 RIKEN full-length enriched, adult male testis Mus musculus
CDNA clone 4930488D08 5', mRNA sequence.
ACCESSION BY715200
VERSION   BY715200.1 GI:27128317
KEYWORDS EST.
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SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 969)
AUTHORS     Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
             Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaoka,I.,
             Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
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             Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE       Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL     Nature 420, 563-573 (2002)
MEDLINE     22354683
PUBMED      12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
            Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
            Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
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            Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
            Direct Submission
            Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
            Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site (http://genome.gsc.riken.go.jp) for
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GAGAGAGAGAGAGATCCAGAGCTTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5',  
GAGAGAGAGAGCGCGCCCAATTAATCTCGAGTTAATTAATATCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites."

ORIGIN

Query Match 96.1%; Score 558.6; DB 6; Length 969;  
Best Local Similarity 97.6%; Pred. No. 9.1e-134;  
Matches 567; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGCCGACCCAGCCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
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RESULT 5  
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ACCESSION BU503850  
VERSION BU503850.1 GI:22810083  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.  
AUTHORS 1 (bases 1 to 967)  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: The Cepko Laboratory  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
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High quality sequence stop: 524.  
Location/Qualifiers

FEATURES  
source

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ORIGIN

Query Match 86.7%; Score 503.6; DB 5; Length 967;  
Best Local Similarity 96.8%; Pred. No. 1.6e-119;  
Matches 567; Conservative 0; Mismatches 14; Indels 5; Gaps 5;

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Db	550	CAGTGGGGGGCTGGGGCGAGTTTACAGCTCTATACGGGGACGGGGCTTGAGGAGCA	609
QY	478	CGGCGTCTGCGGGAGGGCAACTGGGCATGAGTGACACAGTGTGAC-GGGGGCCGTGC	536
Db	610	CGGCGTCTGCGGGAGGGCAACTGGGCATGAGTGAGACAGTGTGACGGGGGGCCGTGC	669
QY	537	ACTGGGGGGCCCTGTACTGT-AGGGGCTTTTGTGTAACAATG	581
Db	670	ACTGGGGGGCCCTGTACTGTAGGGGCTTTTGTGTAACAATG	715
RESULT 6			
LOCUS	AY421020	582 bp	DNA linear
DEFINITION	Homo sapiens BCL2L2 gene, VIRTUAL TRANSCRIPT, partial sequence,		
ACCESSION	AY421020		
VERSION	AY421020.1		
KEYWORDS	GSS.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 582)		
TITLE	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCE	2 (bases 1 to 582)		
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
JOURNAL	This sequence as made by sequencing genomic exons and ordering them based on alignment.		
COMMENT	Location/Qualifiers		
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	/locus_tag="HCM7418"		
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Best Local Similarity	91.4%;	Pred. No. 7e-119;	
Matches 531;	Conservative 0;	Mismatches 50;	Indels 0; Gaps 0;
QY	1	ATGCCGACCCCAAGCCTCAACCCAGACACACGGGCTCTAGTGCTGACTTGTAGGCTAT	60
Db	1	ATGGCGACCCCAAGCCTCGGCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT	60
QY	61	AGGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCAGCCCGAC	120
Db	61	AAGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGCCCGGGGAGGGCCAGCAGCTGAC	120
QY	121	CCGCTGACCAAGCCATGCGGCTGTGAGAGAGTTTGAGACCCGTTCCGCCGAC	180
Db	121	CCACTGCACCAAGCCATGCGGCGAGCTGAGATGAGTTGAGACCCCGCTTCCGCCGAC	180
QY	181	TTCTCTGACTGGCCGCTCAGCTACACGTACCCCAAGGCTCAGCCCAACGCTTACC	240
Db	181	TTCTCTGACTGGCCGCTCAGCTGATGTGACCCCAAGGCTCAGCCCAACGCTTACC	240

QY	241	CAGGTTCCGACGAACTTTTCCAAAGGGGGCCCTAACTGGGGCCGTTGTGGCAATCTTT	300
Db	241	CAGGTTCCGATGAATTTTCAAGGGGGCCCAACTGGGGCCGTTGTAGCCTTCTT	300
QY	301	GTCTTTGGGGCTGCCCCGTGTGCTGTAGAGTGTCAACAAAGAAATGAGCCTTTGGTGGGA	360
Db	301	GTCTTTGGGGCTGCACTGTGTGTGAGAGTGTCAACAAAGAGATGAAACCACTGTTGGA	360
QY	361	CAAGTCCAGGATTGGATCGTGGCCTAAGAGACAGTCTGGCTGACTGATCCACAGC	420
Db	361	CAAGTCAAGAGTGAATGTGTGCTTAAGAGACGCGCTGGCTGACTGATCCACAGC	420
QY	421	AGTGGCGGCTGGCGGACTTCACAGCTCTATACGGGACGGGCCCTGGAGAGCAGCAGG	480
Db	421	AGTGGGGGCTGGGGGAGTTCAAGCTCTATACGGGACGGGCCCTGGAGAGCGCGG	480
QY	481	CGTCTGCGGGAGGGCAACTGGGCAATGAGTGAGCACAGTGTGTACGGGGCCGTGGCACTG	540
Db	481	CGTCTGCGGGAGGGGAACTGGGCAATGAGTGAGCACAGTGTGTACGGGGCCGTGGCACTG	540
QY	541	GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAGTG	581
Db	541	GGGGCCCTGTACTGTAGGGGCTTTTGTCTAGCAAGTG	581
RESULT 7			
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LOCUS	CD617893	727 bp	mRNA linear EST 12-JAN-2004
DEFINITION	56057475J1 FLP Homo sapiens cDNA, mRNA sequence.		
ACCESSION	CD617893		
VERSION	CD617893.1 GI:40266158		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 727)		
AUTHORS	Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.		
TITLE	Circular rapid amplification of cDNA ends for high-throughput		
JOURNAL	Genomics 84 (1), 205-210 (2004)		
COMMENT	Contact: Fu GK		
	Incyte Genomics, Inc.		
	3160 Porter Dr., Palo Alto, CA 94304, USA		
	Tel: 6508454102		
	Email: gfu@incyte.com.		
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Query Match	86.2%;	Score 501;	DB 6; Length 727;
Best Local Similarity	91.4%;	Pred. No. 7.2e-119;	
Matches 531;	Conservative 0;	Mismatches 50;	Indels 0; Gaps 0;
QY	1	ATGCCGACCCCAAGCTTCAACCCAGACACACGCGCTCTAGTGGTGAATTTGTAGGCTAT	60
Db	608	ATGGCGACCCCAAGCTTGGCCCGACACACAGGCGCTCTGTGGCAGACTTTGTAGGTTAT	549
QY	61	AGGCTGAGGCAAGAGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCACGCCCGAC	120
Db	548	AAGCTGAGGCAAGAGGTTATGTCTGTGAGCTGGCCCGGGGAGGGCCACGACTGAC	489
QY	121	CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTCCGCCGAC	180
Db	488	CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTTGAGACCCGCTTCGGCGCACC	429
QY	181	TTCTCTGACCTGGCCGCTCAGCTTACAGTGACCCCGAGGCTCAGCCCAAGCAAGCTTCA	240

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Db 428 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAAGGCTCAGCCCAACACAGCTTCACC 369
Qy 241 CAGGTTCCGACGAACCTTTTCCAAAGGGGGCCCTTAAGTGGGGCCGTCTTGTGGCATTTCTT 300
Db 368 CAGGTCTCCGATGAACCTTTTCAAGGGGGGCCCAACTGGGGCCGCTTGTAGCTTCTTT 309
Qy 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGAGCCTTGTGGGA 360
Db 308 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAAACCACTGTGGGA 249
Qy 361 CAAGTCCAGATTGATCGTGGCCCTACCTGGAGACAGTCTGGCTGACTGGATCCACAGC 420
Db 248 CAAGTGCAAGAGTGAATGTTGGCCCTACCTGGAGACGGGGCTGGCTGACTGGATCCACAGC 189
Qy 421 AGTGGCGGCTGGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGACGCCACGG 480
Db 188 AGTGGGGGCTGGGGCGGAGTTCAACAGCTCTATACGGGGACGGGGCCCTGGAGAGGGCGGG 129
Qy 481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGTGACGGGGCCCTGGCACTG 540
Db 128 CGTCTGCGGGAGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCCTGGCACTG 69
Qy 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581
Db 68 GGGGCACGTGGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTG 28
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RESULT 8
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LOCUS 56057367J1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD617891
ACCESSION CD617891
VERSION CD617891.1 GI:40266156
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 629)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
source 1..629
/organism="Homo sapiens"
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Best Local Similarity 91.2%; Pred. No. 1.8e-118;
Matches 530; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
Qy 1 ATGCCGACCCAGCCTCAACCCAGACACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db 607 ATGGCGACCCAGCCTCGGCCCCAGACACACAGGGCTCTGTGGCAGACTTTGTAGGTTAT 548
Qy 61 AGGCTGAGGCAGAAAGGTTATGTCTGTGAGAGCTGGGCTGGGGAAGGCCCAAGCCCGAGC 120
Db 547 AAGCTGAGGCAGAAAGGTTATGTCTGTGAGAGCTGGGCCCGGGAGAGGCCCAAGCACTGAC 488
Qy 121 CCGCTGACCAAGCAATGCGGGCTGTGAGAGAGTTTGAAGCCCGTTCCGCCGACAC 180
Db 487 CCGCTGACCAAGCAATGCGGGCAGCTGAGATGAGTTTGAAGCCCGCTTCGCCGACAC 428
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Qy 181 TTCTTGACCTGCGCGCTCAGCTACAGTGACGCCAGGCTCAGGCCAGCAACGCTTCACC 240
Db 427 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAAGGCTCAGGCCCAACACGCTTCACC 368
Qy 241 CAGGTTCCGACGAACCTTTTCCAAAGGGGGCCCTTAAGTGGGGCCGTCTTGTGGCATTTCTT 300
Db 367 CAGGTCTCCGATGAACCTTTTCAAGGGGGGCCCAACTGGGGCCGCTTGTAGCTTCTTT 308
Qy 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGAGCCTTGTGGGA 360
Db 307 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAAACCACTGTGGGA 248
Qy 361 CAAGTCCAGATTGATCGTGGCCCTACCTGGAGACAGCTCTGGCTGACTGGATCCACAGC 420
Db 247 CAAGTGCAAGAGTGAATGTTGGCCCTACCTGGAGACGGGGCTGGCTGACTGGATCCACAGC 188
Qy 421 AGTGGCGGCTGGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGACGCCACGG 480
Db 187 AGTGGGGGCTGGGGCGGAGTTCAACAGCTCTATACGGGGACGGGGCCCTGGAGAGGGCGGG 128
Qy 481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGTGACGGGGCCCTGGCACTG 540
Db 127 CGTCTGCGGGAGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCCTGGCACTG 68
Qy 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581
Db 67 GGGCCTCGGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTG 27
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RESULT 9
AL157542 804 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp761D0816 r1 761 (synonym: hamy2) Homo sapiens cDNA clone
DEFINITION DKFZp761D0816 5', mRNA sequence.
ACCESSION AL157542
VERSION AL157542.1 GI:7057943
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 804)
AUTHORS Ansorge, W., Wirkner, U., Mewes, W., Well, B. and Wiemann, S.
TITLE EST (Ansorge, W., Wirkner, U., Mewes, H.W., Well, B. and Wiemann, S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No al sequence available.
This clone (DKFZp761D0816) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source 1..804
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/db_xref="taxon:9606"
/clone="DKFZp761D0816"
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/dev_stage="adult"
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ORIGIN
Query Match 82.2%; Score 477.6; DB 1; Length 804;
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Best Local Similarity 91.0%; Pred. No. 8.5e-113;  
Matches 529; Conservative 0; Mismatches 50; Indels 2; Gaps 2;

QY 1 ATGCCGACCCAGCCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
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QY 61 AGGCTGAGGAGAGGGTATATGTCTGTGAGAGCTGGGCTGGGGAAGGCCAGCCGCGAC 120  
Db 194 AAGCTGAGGAGAGGGTATATGTCTGTGAGAGCTGGGCCCGGGAAGGCCAGCAGCTGAC 253  
QY 121 CCGCTGACCAAGCCATGCGGGCTGTGGAGACGAGTTTGAGACCCGTTCCGCGCAC 180  
Db 254 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGAGTTCGAGACCCGCTTCCGCGCAC 313  
QY 181 TTCTCTGACCTGGCCGCTCAGCTACAGTGAACCCAGGCTCAGCCAGCAACGCTTCACC 240  
Db 314 TTCTCTGATCTGGCGCTCAGCTGATGATGACCCAGGCTCAGCCAGCAACGCTTCACC 373  
QY 241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCGTCTTGTGCAATCTTT 300  
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Db 434 GTCTTTGGGGCTGACATGTGTGNGAGAGTGTCAACAAGAGATGGAACCACTGTGTGGGA 493  
QY 361 CAAGTCCAGGATTGATCGTGCCCTACCTGGAGACAGCTGTGGCTGACTGTGATCCACAGC 420  
Db 494 CAAGTCCAGGAGTGTGATGTGCTTACCTGGAGACCGCGCTGGCTGACTGTGATCCACAGC 553  
QY 421 AGTGGCGGCTGGCGGAGCTTCAACAGCTCTATACGGGGACGGGGCCCTGGAGAGCGCACGG 480  
Db 554 AGTGGGGGCTGGCGGAGTTCAACAGCTCTATACGGGGAC-GGGCCCTGGAGAGGGCGCGG 612  
QY 481 CGTCTCGGGAGGGCACTGGGCATGAGTGAGCACAGTGTGACGGGGCGCTGGCACTG 540  
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QY 541 GGGGCCCTGGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581  
Db 672 GGGGCCCTGGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 712

RESULT 10  
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LOCUS 601590016F1 NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:3944307 5',  
DEFINITION mRNA sequence.  
ACCESSION BE793530  
VERSION BE793530  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 1030)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DRP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
Plate: LNCM800 row: P column: 04  
High quality sequence start: 5  
High quality sequence stop: 709.  
Location/Qualifiers  
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FEATURES  
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/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
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adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 82.1%; Score 477; DB 2; Length 1030;  
Best Local Similarity 88.8%; Pred. No. 1.3e-112;  
Matches 516; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 ATGCCGACCCAGCCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
Db 144 ATGGCGACCCAGCCTCGGCCAGACACACGCGCTCTGTTGGCAGACTTTGTAGGTTAT 203  
QY 61 AGGCTGAGGAGAGGGTATATGTCTGTGAGAGCTGGGCTGGGGAAGGCCAGCCGCGAC 120  
Db 204 AAGCTGAGGAGAGGGTATATGTCTGTGAGAGCTGGGCCCGGGAAGGCCAGCAGCTGAC 263  
QY 121 CCGCTGACCAAGCCATGCGGGCTGTGGAGACGAGTTTGAGACCCGTTCCGCGCAC 180  
Db 264 CCACCTGACCAAGCCATGCGGGCAGCTGAGATGAGTTCGAGACCCGCTTCCGCGCAC 323  
QY 181 TTCTCTGACCTGGCCGCTCAGCTACAGTGAACCCAGGCTCAGCCAGCAACGCTTCACC 240  
Db 324 TTCTCTGATCTGGCGCTCAGCTGATGATGACCCAGGCTCAGCCAGCAACGCTTCACC 383  
QY 241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCGTCTGTGCAATCTTT 300  
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QY 301 GTCTTTGGGGCTGCGCTGTGTGTGAGAGTGTCAACAAGAAATGAGCCCTTGGTGGGA 360  
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QY 361 CAAGTCCAGGATTGATCGTGCCCTACCTGGAGACACGCTGTGGCTGACTGTGATCCACAGC 420  
Db 504 CAAGTCCAGGAGTGTGATGTGCTTACCTGGAGACCGCGCTGGCTGACTGTGATCCACAGC 563  
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Db 564 AGTGGGGGCTGGCGGAGTTCAACAGCTCTATACGGGGAGCGGGCCCTGGAGAGCGCGCG 623  
QY 481 CGTCTCGGGAGGGCACTGGGCATGAGTGAGCACAGTGTGACGGGGCGCTGGCACTG 540  
Db 624 CGTCTCGGGAGGGCACTGGGCATGAGTGAGCACAGTGTGACGGGGCGCTGGCACTG 683  
QY 541 GGGGCCCTGGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581  
Db 684 GGGGCCCTGGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 724

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BP753931 713 bp mRNA linear EST 08-JUL-2004  
LOCUS BP753931  
DEFINITION BP753931 mouse (C57BL/6) pancreatic islet library with  
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mRNA sequence.  
ACCESSION BP753931  
VERSION BP753931.1 GI:50073821  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)



ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 713)  
AUTHORS Nishimura, M., Yokoi, N., Miki, T., Horikawa, Y., Yoshioke, H.,  
Takeda, J., Ohara, O. and Seino, S.  
TITLE Construction of a multi-functional cDNA library specific for mouse  
pancreatic islets and its application to microarray  
JOURNAL Unpublished (2004)  
COMMENT Contact: Susumu Seino  
Division of Cellular and Molecular Medicine  
Kobe University Graduate School of Medicine  
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan  
Tel: 81-78-382-5360  
Fax: 81-78-382-5370  
Email: seino@med.kobe-u.ac.jp.

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/dev\_stage="adult"  
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recombination-based method"

ORIGIN  
Query Match 81.1%; Score 471.2; DB 5; Length 713;  
Best Local Similarity 95.3%; Pred. No. 3.8e-111;  
Matches 551; Conservative 0; Mismatches 18; Indels 9; Gaps 6;

QY 2 TGCCGACCCAGCCTCAACCCAGACACACGCGCTTAGTGCTGACTTTGAGGCTATA 61  
DB 34 TGGCGACCCAGCCTCAACCCAGACACACGCGCTTAGTGCTGACTTTGAGGCTATA 93  
QY 62 GGCTGAGGCAAGGGTTATGTCTGTGAGAGTGGCCCTGGGGAGAGGCCCGCCGACC 121  
DB 94 AGCTGAGGCAAGGGTTATGTCTGTGAGAGTGGCCCTGGGGAGAGGCCCGCCGACC 153  
QY 122 CGCTGACCAAGCCATGCGGCTGCTGAGAGAGTTGAGACCCGTTCCGCCGACCT 181  
DB 154 CGCTGACCAAGCCATGCGGCTGCTGAGAGAGTTGAGACCCGTTCCGCCGACCT 213  
QY 182 TCTGTACCTGGCGCTCAGCTACACGTGAGCCAGGCTCAGCCAGCAAGCTTCACCC 241  
DB 214 TCTGTACCTGGCGCTCAGCTACACGTGAGCCAGGCTCAGCCAGCAAGCTTCACCC 273  
QY 242 AGGTTCCGACGAACTTTTCCAGAGGGGCGCTAACTGGGGCGCTTGTGGCACTTTG 301  
DB 274 AGGTTCCGACGAACTTTTCCAGAGGGGCGCTAACTGGGGCGCTTGTGGCACTTTG 333  
QY 302 TCTTTGGGGCTG-CCTGTGTGTGAGAGTGAAC-AAAGAATGAGCCTTTGG--TG 357  
DB 334 TCTTTGGGGCTGCCCCCTGTGTGTGAGAGTGAACAAAGAATGAGCCTTTGGGTGG 393  
QY 358 GGACAAGTCCAGATTGG--ATCGTGGCGCTTACT-GGAGACACGCTTGGCTGACTGATC 414  
DB 394 GGACAAGTCCAGATTGGGATGGGTGGCTTACTGGGAGACACGCTTGGCTGACTGATC 453  
QY 415 CACAGCAGTGGCG--CTGGGCGGACTTACAGCTCTATACGGGGGAGCGGGGCCCTGAGG 472  
DB 454 CACAGCAGTGGGGGCTGGGGCGGAGTTACAGCTCTATACGGGGGAGCGGGGCCCTGAGG 513  
QY 473 ACGCAGCGGCTGTGCGGAGAGGGCAACTGGGCAATGAGTGAGCAGAGTGTGACGGGGCGG 532  
DB 514 AGGCACGGGCTGTGCGGAGAGGGGAAGTGGGCACTGAGGAGACAGTGTGACGGGGCGG 573  
QY 533 TGGCACTGGGGCGCTGTGTAAGTGTAGGGGCTTTT 570  
DB 574 TGGCACTGGGGCGCTGTGTAAGTGTAGGGGCTTTT 611

RESULT 12  
CK359685 757 bp mRNA linear EST 23-DEC-2003  
LOCUS CK359685  
DEFINITION AGENCOURT 17156314 NIH\_MGC 233 Rattus norvegicus cDNA clone  
IMAGE:7105621 5', mRNA sequence.  
ACCESSION CK359685  
VERSION CK359685.1 GI:40325617  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 757)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgabds-r@mail.nih.gov  
Tissue Procurement: Howard Jacobs  
cDNA Library Preparation: Express Genomics  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LLM14965 row: a column: 11  
High quality sequence start: 20  
High quality sequence stop: 702.

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1. 757  
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/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="IMAGE:7105621"  
/tissue\_type="heart, pooled"  
/lab\_host="DH10B Tona"  
/clone\_lib="NIH\_MGC 233"  
/note="Organ: heart; Vector: pExpress-1; Site 1: EcoRV;  
Site 2: NotI; RNA obtained from pooled heart tissue from a  
mix of male and female animals at 8 wk old. Tissues were  
snap-frozen and kept at -80C for two days before RNA  
extraction and purification (Tri-reagent method). cDNA was  
primed using oligo-dT primer:  
5'-pgACTAGTCTAGATCGGAGCGGCGCC(T)25-3' and cloned into  
the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb  
resulted in an average insert size of 2 kb. This primary  
library is not normalized (normalized primary library is  
NIH\_MGC 234) and was constructed by Express Genomics  
(Frederick, MD). Note: this is a NIH\_MGC library."

ORIGIN  
Query Match 78.6%; Score 456.6; DB 7; Length 757;  
Best Local Similarity 95.9%; Pred. No. 2.3e-107;  
Matches 490; Conservative 0; Mismatches 19; Indels 2; Gaps 2;

QY 1 ATGCCGACCCAGCCTCAACCCAGACACACGCGCTAGTGCTGACTTTGAGGCTAT 60  
DB 233 ATGCCGACCCAGCCTCAACCCAGACACACGCGCTAGTGCTGACTTTGAGGCTAT 292  
QY 61 AGCTGAGGCAAGAGGTTATGTCTGTGAGAGCTGGGCTGGGGAAGGCCAGCCGCGAC 120  
DB 293 AAGCTGAGGCAAGAGGTTATGTCTGTGAGAGCTGGGCTGGGGAAGGCCAGCCGCGAC 352  
QY 121 CCGCTGACCAAGCCATGCGGCTGCTGAGAGAGAGTTTGAGACCCGTTCCGCGCAC 180  
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QY	301	GTCCTTGGGGCTGCGCTGTGTGCTGAGATGTCAACAAGAAATGAGCCTTGTGGGA	360
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QY	361	CAAGTCCAGGATTGGATCGTGGCGCTACCTGGAGACACGCTTGGGCTGACTGATCCACAGC	420
Db	593	CAAGTCCAGGATTGGATGATGTGACTTACCTGGAGACACGCTTGGGCTGACTGATCCACAGC	652
QY	421	AGTGGCGGCTGGGCGGACTTCAACAGCTCTATACGGGGACGGGGCGCTGGAGGACGCCACGG	480
Db	653	AGTGGGGGCTGGGCGGAGTTCAACAGCTCTATACGGGGACGGGGCGCTGGAGGA-GCACGG	711
QY	481	CGTCTCGGGAGGGCAACTGGGCGATGAGTGA	511
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LOCUS	CN281020 643 bp mRNA linear EST 16-MAY-2004
DEFINITION	17000531876837 GRN_EB Homo sapiens CDNA 5', mRNA sequence.
ACCESSION	CN281020
VERSION	CN281020.1 GI:47297434
KEYWORDS	EST.
SOURCE	Homo sapiens (human)

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 643)	Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.	Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation	Nat. Biotechnol. 22 (6), 707-716 (2004)

TITLE	Transcriptome characterization elucidates signal control human ES cell growth and differentiation
JOURNAL	Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT	Contact: Brandenberger R Regenerative Medicine Geron Corporation 230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658 Fax: 650 473 7760 Email: rbrandenberger@geron.com Insert Length: 643 Std Error: 0.00.

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derived from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
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from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

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ORIGIN	CONNECTIONS
Query Match	78.5%; Score 456; DB 7; Length 643;
Best Local Similarity	90.7%; Pred. No. 3.2e-107;
Matches 486; Conservative	0; Mismatches 50; Indels 0; Gaps 0;

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 Ddb 108 ATGCGACACCCCGAGCCTCGGCCCCGAGACACGCGGCTCTGCTGGCAGACTTTGTAGGTTAT 160  
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QY	61	AGGCTGAGGGCAGAAAGGGTTATGTCGTGAGCTGGGCCCTGGGGAAAGGCCAGCCGCCGAC	120
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Db	348	CAGGTTCTCCGATGAACCTTTTCCAAGGGGGCCCAACTGGGCGCTTGTAGCCTTCTTT	407
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Db	408	GTCCTTGGGGCTGCACGTGTGTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA	467
QY	361	CAAGTCCAGGATTGATTCGTGGCCTACCTGGAGACACGCTGTGGCTGACTGGATCCACAGC	420
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RESULT	14
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LOCUS	662 bp
DEFINITION	mRNA linear
ACCESSION	56057475SH1 FLP Homo sapiens CDNA, mRNA sequence.
VERSION	CD617892.1 GI:40266157

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 662)
AUTHORS	Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE	Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL	Genomics 84 (1), 205-210 (2004)
COMMENT	Contact: Fu GK

3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.

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FEATURES
source
location/Qualifiers
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/organism="Homo sapiens"
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Query Match	77.1%;	Score 447.8;	DB 6;	length 662;
Best Local Similarity	90.2%;	Pred. No. 4.3e-105;		
Matches 490; Conservative	0;	Mismatches 52;	Indels 1;	Gaps 1;

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Db 120 ATGGCGACCCCGAGCCTCGGCCCCAGACACACGGGCTCTGGTGCCAGACTTTGTAGTTAT 179  
QY 61 AGGCTGAGGCAGAGGGTTATCTGTGAGCTGGGCGCTGGGGAAGGCCAGCGCGGCAC 120

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Qy 361 CAAGTCCAGGATTGGA-TGCTGGCCTTACCTGAGACACAGTCTGCTGATGATCCACAG 419
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Qy 480 GCGTCTGCGGGAGGGCAACTGGGCATGATGAGCAACAGTGTGACGGGGGCCCTGGCACT 539
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Qy 540 GGG 542
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## RESULT 15

CD617890

LOCUS CD617890 627 bp mRNA linear EST 12-JAN-2004  
DEFINITION 56057367H1 FLP Homo sapiens cDNA, mRNA sequence.

ACCESSION CD617890

VERSION CD617890.1 GI:40266155

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 627)  
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
JOURNAL Genomics 84 (1), 205-210 (2004)  
COMMENT Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.

## FEATURES

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/mol\_type="mRNA"  
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## ORIGIN

Query Match 74.5%; Score 432.8; DB 6; Length 627;  
Best Local Similarity 90.7%; Pred. No. 3.3e-101;  
Matches 461; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
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Db 120 ATGGCGACCCCAAGCTTCGGCCCAAGACACAGCGGCTCTGTGGCAGACTTTGTAGGTTAT 179

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Qy 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGCCCTGGGGAAAGGCCAGCCCGGAC 120
Db 180 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGGCCCCGGGAGGGGCCCAAGCAGCTGAC 239
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Db 240 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGCTCCGGCGCACC 299
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Qy 241 CAGGTTCCGACGAATTTCGAAGGGGCCCTTAAGTGGGCCGCTTGTGGCATTCTTT 300
Db 360 CAGGTTCCGATGAATTTTCAAGGGGGCCCCCAACTGGGGCCGCTTGTAGCCTTCTT 419
Qy 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGAGCCTTTGGTGGGA 360
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Qy 421 AGTGGCGGCTGGCGGCACTTCAACAGCTCTATACGGGGACGGGCCCTTGAAGACGACG 480
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Qy 481 CGTCTGCGGGAGGGCAACTGGGCATGAG 508
Db 600 CGTCTGCGGGAGGGGAAGTGGGCATGAG 627
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Job time : 2833.63 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2005, 22:21:58 ; Search time 19.5 Seconds  
(without alignments)  
738.834 Million cell updates/sec

Title: US-09-925-674B-9  
Perfect score: 1009  
Sequence: 1 MATPASTPDTRALVADFGVY.....LTGAVALGALVTGAFPAASK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1009	100.0	193	4	US-09-155-327G-9 Sequence 9, Appli
2	1005	99.6	193	1	US-08-798-897-3 Sequence 3, Appli
3	1005	99.6	193	2	US-08-978-523-3 Sequence 3, Appli
4	1000	99.1	192	1	US-08-798-897-5 Sequence 5, Appli
5	1000	99.1	192	2	US-08-978-523-5 Sequence 5, Appli
6	1000	99.1	193	4	US-09-155-327G-7 Sequence 7, Appli
7	1000	99.1	193	4	US-09-949-016-10928 Sequence 10928, A
8	995	98.6	193	1	US-08-798-897-4 Sequence 4, Appli
9	995	98.6	193	2	US-08-798-523-4 Sequence 6, Appli
10	990	98.1	192	1	US-08-798-897-6 Sequence 6, Appli
11	990	98.1	192	2	US-08-978-523-6 Sequence 6, Appli
12	776	76.9	333	4	US-09-155-327G-10 Sequence 10, Appli
13	759	75.2	365	4	US-09-149-476-696 Sequence 696, App
14	759	75.2	365	4	US-09-010-147B-24 Sequence 24, Appli
15	432.5	42.9	411	4	US-09-639-245-2 Sequence 2, Appli
16	428.5	42.5	233	3	US-09-271-014A-6 Sequence 6, Appli
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19	427.5	42.4	233	1	US-08-607-269-24 Sequence 24, Appli
20	427.5	42.4	233	1	US-08-471-058-14 Sequence 14, Appli
21	427.5	42.4	233	2	US-08-661-479-59 Sequence 59, Appli
22	427.5	42.4	233	2	US-08-470-670A-7 Sequence 14, Appli
23	427.5	42.4	233	3	US-08-471-057-14 Sequence 14, Appli
24	427.5	42.4	233	3	US-08-481-739-2 Sequence 2, Appli
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41	411.5	40.8	239	2	US-08-856-531-10	Sequence 10, Appli
42	411.5	40.8	239	2	US-08-856-034-10	Sequence 10, Appli
43	411.5	40.8	239	3	US-09-127-048-8	Sequence 8, Appli
44	411.5	40.8	239	3	US-08-927-326-10	Sequence 10, Appli
45	411.5	40.8	239	4	US-09-379-820A-10	Sequence 10, Appli

ALIGNMENTS

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RESULT 1
US-09-155-327G-9
; Sequence 9, Application US/09155327G
; Patent No. 6790637
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
; FILE REFERENCE: 2096584
; CURRENT APPLICATION NUMBER: US/09/155,327G
; CURRENT FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Mouse
US-09-155-327G-9

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DB      181 GALVTGAFPAASK 193

RESULT 2
US-08-798-897-3
; Sequence 3, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
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; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-798-897-3

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Db 181 GALVTGAFPAK 193

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RESULT 3
US-08-978-523-3
; Sequence 3, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-978-523-3

```

```

Query Match          99.6%; Score 1005; DB 2; Length 193;
Best Local Similarity 99.5%; Pred. No. 8.5e-107;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDTRALVADFGVGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRT 60
Db 1 MATPASTPDTRALVADFGVGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHVTTPGSAQORFTQVSDELFGGGPNWGRVLAFFVFGALCAESVNKEMEPLVG 120
Db 61 FSDLAQLHVTTPGSAQORFTQVSDELFGGGPNWGRVLAFFVFGALCAESVNKEMEPLVG 120
QY 121 QVQDMWVYLETRLADWIHSSGGWAEFTALYGDGALAEARRLREGNWSVRYTLTGAVAL 180
Db 121 QVQDMWVYLETRLADWIHSSGGWAEFTALYGDGALAEARRLREGNWSVRYTLTGAVAL 180
QY 181 GALVTGAFPAK 193
Db 181 GALVTGAFPAK 193

```

```

RESULT 4
US-08-798-897-5
; Sequence 5, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```

NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 192 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-798-897-5

Query Match 99.1%; Score 1000; DB 1; Length 192;  
Best Local Similarity 99.5%; Pred. No. 3.2e-106;  
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATPASTPTTRALVADFVGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRTF 61  
DB 1 ATPASTPTTRALVADFVGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRTF 60  
QY 62 SDLAQLHVTTPGSAQQRFTQVSDELFOGQPNWGRLVAFVFGAALCAESVKNKMEPLVGQ 121  
DB 61 SDLAQLHVTTPGSAQQRFTQVSDELFOGQPNWGRLVAFVFGAALCAESVKNKMEPLVGQ 120  
QY 122 VQDMWVAYLETRLADWIHSSGGWAEFTALYGDALBEARLRREGNWSVRTLGTGAVALG 181  
DB 121 VQDMWVAYLETRLADWIHSSGGWAEFTALYGDALBEARLRREGNWSVRTLGTGAVALG 180  
QY 182 ALVTVGAFPAASK 193  
DB 181 ALVTVGAFPAASK 192

## RESULT 5

US-08-978-523-5  
Sequence 5, Application US/08978523  
Patent No. 5883229  
GENERAL INFORMATION:  
APPLICANT: Guateella, John  
TITLE OF INVENTION: Genes Coding for Bcl-Y, a Bcl-2  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,523  
FILING DATE: herewith  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 192 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-978-523-5

Query Match 99.1%; Score 1000; DB 2; Length 192;  
Best Local Similarity 99.5%; Pred. No. 3.2e-106;  
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATPASTPTTRALVADFVGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRTF 61  
DB 1 ATPASTPTTRALVADFVGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRTF 60  
QY 62 SDLAQLHVTTPGSAQQRFTQVSDELFOGQPNWGRLVAFVFGAALCAESVKNKMEPLVGQ 121  
DB 61 SDLAQLHVTTPGSAQQRFTQVSDELFOGQPNWGRLVAFVFGAALCAESVKNKMEPLVGQ 120  
QY 122 VQDMWVAYLETRLADWIHSSGGWAEFTALYGDALBEARLRREGNWSVRTLGTGAVALG 181  
DB 121 VQDMWVAYLETRLADWIHSSGGWAEFTALYGDALBEARLRREGNWSVRTLGTGAVALG 180  
QY 182 ALVTVGAFPAASK 193  
DB 181 ALVTVGAFPAASK 192

## RESULT 6

US-09-155-327G-7  
Sequence 7, Application US/09155327G  
Patent No. 6790637  
GENERAL INFORMATION:  
APPLICANT: AMRAD Operations Pty Ltd  
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2  
TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES  
FILE REFERENCE: 2096584  
CURRENT APPLICATION NUMBER: US/09/155,327G  
CURRENT FILING DATE: 1999-03-29  
PRIOR APPLICATION NUMBER: PN8965  
PRIOR FILING DATE: 1996-03-27  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 193  
TYPE: PRT  
ORGANISM: HUMAN  
US-09-155-327G-7

Query Match 99.1%; Score 1000; DB 4; Length 193;  
Best Local Similarity 99.0%; Pred. No. 3.2e-106;  
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTTRALVADFVGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASTPTTRALVADFVGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAQLHVTTPGSAQQRFTQVSDELFOGQPNWGRLVAFVFGAALCAESVKNKMEPLVG 120  
DB 61 FSDLAQLHVTTPGSAQQRFTQVSDELFOGQPNWGRLVAFVFGAALCAESVKNKMEPLVG 120  
QY 121 VQDMWVAYLETRLADWIHSSGGWAEFTALYGDALBEARLRREGNWSVRTLGTGAVAL 180  
DB 121 VQDMWVAYLETRLADWIHSSGGWAEFTALYGDALBEARLRREGNWSVRTLGTGAVAL 180  
QY 181 GALVTVGAFPAASK 193  
DB 181 GALVTVGAFPAASK 193

## RESULT 7

US-09-949-016-10928

```

; Sequence 10928, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10928
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10928

```

```

Query Match          99.1%; Score 1000; DB 4; Length 193;
Best Local Similarity 99.0%; Pred. No. 3.2e-106;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MATPASTPDTRALVADFGVGYKLRQKGYCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60
Db 1 MATPASAPDTRALVADFGVGYKLRQKGYCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAQQLHVTTPGSAQQRFTQVSDLEFQGGPNWGRVAFVFGAALCAESVNKEMEPLVG 120
Db 61 FSDLAQQLHVTTPGSAQQRFTQVSDLEFQGGPNWGRVAFVFGAALCAESVNKEMEPLVG 120
QY 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTVLTGAVAL 180
Db 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTVLTGAVAL 180
QY 181 GALVTVGAFPFASK 193
Db 181 GALVTVGAFPFASK 193

```

```

RESULT 8
US-08-798-897-4
; Sequence 4, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-798-897-4

```

```

Query Match          98.6%; Score 995; DB 1; Length 193;
Best Local Similarity 98.4%; Pred. No. 1.2e-105;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MATPASTPDTRALVADFGVGYKLRQKGYCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60
Db 1 MATPASAPDTRALVADFGVGYKLRQKGYCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAQQLHVTTPGSAQQRFTQVSDLEFQGGPNWGRVAFVFGAALCAESVNKEMEPLVG 120
Db 61 FSDLAQQLHVTTPGSAQQRFTQVSDLEFQGGPNWGRVAFVFGAALCAESVNKEMEPLVG 120
QY 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTVLTGAVAL 180
Db 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTVLTGAVAL 180
QY 181 GALVTVGAFPFASK 193
Db 181 GALVTVGAFPFASK 193

```

```

RESULT 9
US-08-978-523-4
; Sequence 4, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid

```



STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-978-523-4

Query Match 98.6%; Score 995; DB 2; Length 193;  
Best Local Similarity 98.4%; Pred. No. 1.2e-105;  
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASTPDTRALVADFGVGYKLROKGYVCGAGPGEGBPAADPLHQAMRAAGDEFEFRRT 60  
DB 1 MATPASAPDTRALVEDFGVGYKLROKGYVCGAGPGEGBPAADPLHQAMRAAGDEFEFRRT 60  
QY 61 FSDLAQLHTTPGSAQORFTQVSDELFOGCPNMGRLVAFVFGAALCAESVKNKMEPLVG 120  
DB 61 FSDLAQLHTTPGSAQORFTQVSDELFOGCPNMGRLVAFVFGAALCAESVKNKMEPLVG 120  
QY 121 QVQDMWVAYLETRLADWIHSSGWAFFETALYGDGALBEARRLREGNMAASVRTLGTGAVAL 180  
DB 121 QVQDMWVAYLETRLADWIHSSGWAFFETALYGDGALBEARRLREGNMAASVRTLGTGAVAL 180  
QY 181 GALVTGAFPAASK 193  
DB 181 GALVTGAFPAASK 193

RESULT 10

US-08-798-897-6  
Sequence 6, Application US/08798897  
Patent No. 5789201  
GENERAL INFORMATION:  
APPLICANT: Guastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
TITLE OF INVENTION: Homologue  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 192 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-798-897-6

Query Match 98.1%; Score 990; DB 1; Length 192;  
Best Local Similarity 98.4%; Pred. No. 4.4e-105;  
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATPASTPDTRALVADFGVGYKLROKGYVCGAGPGEGBPAADPLHQAMRAAGDEFEFRRT 61  
DB 2 ATPASTPDTRALVADFGVGYKLROKGYVCGAGPGEGBPAADPLHQAMRAAGDEFEFRRT 61

DB 1 ATPASAPDTRALVEDFGVGYKLROKGYVCGAGPGEGBPAADPLHQAMRAAGDEFEFRRT 60  
QY 62 SDLAQLHTTPGSAQORFTQVSDELFOGCPNMGRLVAFVFGAALCAESVKNKMEPLVGQ 121  
DB 61 SDLAQLHTTPGSAQORFTQVSDELFOGCPNMGRLVAFVFGAALCAESVKNKMEPLVGQ 120  
QY 122 VQDMWVAYLETRLADWIHSSGWAFFETALYGDGALBEARRLREGNMAASVRTLGTGAVALG 181  
DB 121 VQDMWVAYLETRLADWIHSSGWAFFETALYGDGALBEARRLREGNMAASVRTLGTGAVALG 180  
QY 182 ALVTGAFPAASK 193  
DB 181 ALVTGAFPAASK 192

RESULT 11

US-08-978-523-6  
Sequence 6, Application US/08978523  
Patent No. 583229  
GENERAL INFORMATION:  
APPLICANT: Guastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
TITLE OF INVENTION: Homologue  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,523  
FILING DATE: herewith  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 192 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-978-523-6

Query Match 98.1%; Score 990; DB 2; Length 192;  
Best Local Similarity 98.4%; Pred. No. 4.4e-105;  
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATPASTPDTRALVADFGVGYKLROKGYVCGAGPGEGBPAADPLHQAMRAAGDEFEFRRT 61  
DB 1 ATPASAPDTRALVEDFGVGYKLROKGYVCGAGPGEGBPAADPLHQAMRAAGDEFEFRRT 60  
QY 62 SDLAQLHTTPGSAQORFTQVSDELFOGCPNMGRLVAFVFGAALCAESVKNKMEPLVGQ 121  
DB 61 SDLAQLHTTPGSAQORFTQVSDELFOGCPNMGRLVAFVFGAALCAESVKNKMEPLVGQ 120  
QY 122 VQDMWVAYLETRLADWIHSSGWAFFETALYGDGALBEARRLREGNMAASVRTLGTGAVALG 181

Db 121 VOEWNVAYLETRLADWIHSSGNAEFTALYDGALEEARLREGNWSVRTVLTGAVALG 180  
Qy 182 ALVTGAFASK 193  
Db 181 ALVTGAFASK 192

RESULT 12

US-09-155-327G-10  
; Sequence 10, Application US/09155327G  
; Patent No. 6790637  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2  
; FILE REFERENCE: 2096584  
; CURRENT APPLICATION NUMBER: US/09/155,327G  
; CURRENT FILING DATE: 1999-03-29  
; PRIOR APPLICATION NUMBER: PN8965  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 333  
; TYPE: PRT  
; ORGANISM: murine  
US-09-155-327G-10

Query Match 76.9%; Score 776; DB 4; Length 333;  
Best Local Similarity 75.4%; Pred. No. 3e-80;  
Matches 159; Conservative 5; Mismatches 17; Indels 30; Gaps 4;

Qy 1 MATPASTPDRALVADFGVGYKLRQKGYCGAGPGEPAADPLHQAAMRAAGDEFETRRRT 60  
Db 1 MATPASTPDRALVADFGVGYKLRQKGYCGAGPGEPAADPLHQAAMRAAGDEFETRRRT 60  
Qy 61 FSDLAOLHTPGSAQQRFTQVSDDELFOGGPNMGRVAFVFGAALCAESVKNEMPLVG 120  
Db 61 FSDLAOLHTPGSAQQRFTQVSDDELFOGGPNMGRVAFVFGAALCAESVKNEMPLVG 120  
Qy 121 QVQDMWVAYLETRLADWIHSSGNAEFTALYG-DGALBEARLRRE----- 164  
Db 121 QVQDMWVAYLETRLADWIHSSGNAEFTALYG-DGALBEARLRRE----- 164  
Qy 165 -GN-----WASVRTVLTGAVALGA 182  
Db 180 PGNAGPVIMSLERKMEADARSIVGNVDYGA 210

RESULT 13

US-09-149-476-696  
; Sequence 696, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,336

; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,633  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,583  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,500  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,587  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,492  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,598  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,613  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,582  
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; EARLIER FILING DATE: 1997-05-23  
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; EARLIER FILING DATE: 1997-06-06

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EARLIER APPLICATION NUMBER: 60/047,501

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EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
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EARLIER FILING DATE: 1997-08-22  
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EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 75.2%; Score 759; DB 4; Length 365;  
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DB 61 FSDLAQLHTVTPGSAQQRFTQVSDLEFGGPNWGRVLVAFVFGAALCAESVKNKMEPLVG 120  
QY 121 QVQDMWVAVIETRLADWIHSSGGW 144  
DB 121 QVQDMWVAVIETRLADWIHSSGGW 144

RESULT 14  
US-09-010-147B-24  
Sequence 24, Application US/09010147B  
Patent No. 6653445  
GENERAL INFORMATION:  
APPLICANT: NI et al.  
TITLE OF INVENTION: Human Proteins  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC  
compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,147B  
FILING DATE: 12-NO. 6653445-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,205  
FILING DATE: 21-JAN-1997  
APPLICATION NUMBER: US 60/034,204  
FILING DATE: 21-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Jonathan L. Klein  
REGISTRATION NUMBER: 41,119  
REFERENCE/DOCKET NUMBER: PF353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 365 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
US-09-010-147B-24

Query Match 75.2%; Score 759; DB 4; Length 365;  
Best Local Similarity 98.6%; Pred. No. 3e-78;  
Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDTRALVADFGVGYKLRQKGYVCGAGPGEGPADPLHQAMRAGDEFETRRRT 60  
Db 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEGPADPLHQAMRAGDEFETRRRT 60  
QY 61 FSDLAQLHVTGPSAQQRFTQVSDLEFQGGPNMGRLVAFVFGAALCAESVKNEMEPLVG 120  
Db 61 FSDLAQLHVTGPSAQQRFTQVSDLEFQGGPNMGRLVAFVFGAALCAESVKNEMEPLVG 120  
QY 121 QVQDMVMVAYLETRLADWIHSSGCW 144  
Db 121 QVQDMVMVAYLETRLADWIHSSGCW 144

RESULT 15  
US-09-639-245-2  
Sequence 2, Application US/09639245  
Patent No. 6737511  
GENERAL INFORMATION:  
APPLICANT: Youle et al.  
TITLE OF INVENTION: RECEPTOR-MEDIATED UPTAKE OF AN EXTRACELLULAR BCL-XL  
TITLE OF INVENTION: FUSION PROTEIN INHIBITS APOPTOSIS  
FILE REFERENCE: 4239-55417  
CURRENT APPLICATION NUMBER: US/09/639,245  
PRIOR FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: 60/149,220  
PRIOR FILING DATE: 1999-08-16  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 411  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: genetic fusion  
US-09-639-245-2

Query Match 42.9%; Score 432.5; DB 4; Length 411;  
Best Local Similarity 39.9%; Pred. No. 8.2e-41;  
Matches 93; Conservative 26; Mismatches 63; Indels 51; Gaps 4;

QY 11 RALVADFGVGYKLRQKGY-----VCGAGP-----GEGPAA 39  
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QY 40 D-----PLHQAMRAAGDEFETRRRTFSDLAQLHVTGPSAQQRFTQ 81

Db 86 NGATAHSSSLDAREVI PMAAVKQALREAGDEFELRYRRAFSDLTSQIHITPGTAYQSFEQ 145  
QY 82 VSDELFOGGPNMGRLVAFVFGAALCAESVKNEMEPLVGQVQDMVMVAYLETRLADWIHSS 141  
Db 146 VVNELFRDGVNMGRIVAFSFGALCVESVDKEMQVLVSRIAAMWATYLNHLEPWIQEN 205  
QY 142 GGMABFTALYGDGALLEARLRE--GNMASVRTVLTGAVALGALVTVGAFEFAS 192  
Db 206 GGMDTFVELYGNNAAAESRKQGERFNRNFLTGMTVAGVLLGSLFSRKAYSAA 258

Search completed: April 10, 2005, 22:45:27  
Job time : 19.5 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2005, 20:17:32 ; Search time 59 Seconds  
(without alignments)  
1675.106 Million cell updates/sec

Title: US-09-925-674B-9  
Perfect score: 1009  
Sequence: 1 MATPASTPTDTRALVADFGVY.....LTGAVALGALVTGAFPAASK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1009	100.0	193	1 BCLW_MOUSE	P70345 mus musculu
2	1005	99.6	193	2 O88996	O88996 rattus norv
3	1005	99.6	219	2 Q7TS60	Q7TS60 rattus norv
4	1000	99.1	193	1 BCLW_HUMAN	Q92843 homo sapien
5	996	98.7	192	2 Q6A093	Q6A093 mus musculu
6	960	95.1	193	2 Q8CGL4	Q8CGL4 mus musculu
7	770	76.3	178	2 Q8CFR2	Q8CFR2 mus musculu
8	770	76.3	178	2 Q9CYW5	Q9CYW5 mus musculu
9	655.5	65.0	188	2 Q6GP82	Q6GP82 xenopus lae
10	650.5	64.5	228	1 ARI_XENLA	Q91827 xenopus lae
11	439.5	43.6	233	2 Q9MYW4	Q9MYW4 oryctolagus
12	432.5	42.9	229	1 BCLX_CHICK	Q07816 gallus gall
13	432.5	42.9	233	2 Q8SQ42	Q8SQ42 felis silve
14	431.5	42.8	233	1 BCLX_PIG	Q77737 sus scrofa
15	431.5	42.8	233	2 Q9N1A2	Q9N1A2 sus scrofa
16	428.5	42.5	233	1 BCLX_MOUSE	Q64373 mus musculu
17	428.5	42.5	233	1 BCLX_RAT	P53563 rattus norv
18	428.5	42.5	233	2 Q9MZS7	Q9MZS7 ovis aries
19	427.5	42.4	233	1 BCLX_HUMAN	Q07817 homo sapien
20	427.5	42.4	233	2 Q76LT7	Q76LT7 canis fami1
21	423.5	42.0	233	1 BCL2_CHICK	Q00709 gallus gall
22	415.5	41.2	229	1 BCL2_BOVIN	O02718 bos taurus
23	413	40.9	236	1 BCL2_RAT	P49950 rattus norv
24	412	40.8	236	1 BCL2_MOUSE	P10417 mus musculu
25	412	40.8	236	2 Q7TSN8	Q7TSN8 rattus norv
26	412	40.8	236	2 Q8BQK4	Q8BQK4 mus musculu
27	411.5	40.8	239	1 BCL2_HUMAN	P10415 homo sapien
28	406	40.2	79	2 Q7TS61	Q7TS61 rattus norv
29	402	39.8	236	1 BCL2_CRILLO	Q919v8 cricetulus
30	401.5	39.8	239	2 Q7SSV7	Q7SSV7 canis fami1
31	401	39.7	180	2 Q9BDD5	Q9BDD5 bos taurus

32	401	39.7	217	2 Q99N35	Q99N35 mus musculu
33	400	39.6	238	2 Q90Z98	Q90Z98 brachydanio
34	398.5	39.5	180	2 Q9BDX7	Q9BDX7 bos taurus
35	398	39.4	236	2 Q923R6	Q923R6 cricetulus
36	396.5	39.3	201	2 Q6GLI5	Q6GLI5 xenopus tro
37	395.5	39.2	235	2 Q8I008	Q8I008 felis silve
38	395	39.1	236	2 Q6R755	Q6R755 canis fami1
39	380.5	37.7	284	2 Q7TS62	Q7TS62 rattus norv
40	374.5	37.1	188	2 Q9QWX2	Q9QWX2 mus musculu
41	374.5	37.1	235	2 Q35843	Q35843 mus musculu
42	372.5	36.9	188	2 Q9H1R6	Q9H1R6 homo sapien
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ALIGNMENTS

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BCLW\_MOUSE  
ID BCLW\_MOUSE STANDARD, PRT, 193 AA.  
AC P70345;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Apoptosis regulator Bcl-W (Bcl-2-like 2 protein).  
GN Name=Bcl2l2; Synonyms=Bclw;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96358615; Pubmed=8761287;  
RA Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,  
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.,  
RT "bcl-w, a novel member of the bcl-2 family, promotes cell survival."  
RL Oncogene 13:665-675(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/10J;  
RX MEDLINE=98160183; Pubmed=9500547;  
RA Ross A.J., Waymire K.G., Moss J.E., Parlow A.F., Skinner M.K.,  
RA Russell L.D., Macgregor G.R.;  
RT "Testicular degeneration in Bclw-deficient mice."  
RL Nat. Genet. 18:251-256(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=22354683; Pubmed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,  
RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gibel C., Godzik A., Gough J.,  
RA Grimmond S., Guenrich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., Kling B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Naita K., Okido T., Pavan W.J., Perlee G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

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RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
CC -1- FUNCTION: Promotes cell survival.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and
CC in a wide range of tissues, with highest levels in brain, colon,
CC and salivary gland.
CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC function.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U59746; AAB09056.1; -.
DR EMBL; AF030769; AAB86430.1; -.
DR EMBL; AK015644; BAB39912.1; -.
DR HSSP; Q92843; 100L.
DR MGD; MGI:108052; Bcl2l2.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006915; P:apoptosis; IDA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
KW Apoptosis.
FT DOMAIN 9 29 BH4.
FT DOMAIN 85 104 BH1.
FT DOMAIN 136 151 BH2.
SQ SEQUENCE 193 AA; 20790 MW; 36CA185F5945DFB4 CRC64;
Query Match 100.0%; Score 1009; DB 1; Length 193;
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Db 1 MATPASTPTDTRALVADFGYKLRQKGYVCGAGPGEGPAPADPLHQAMRAAGDEFETRFRRT 60
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Db 61 FSDLAALHTVPGSAQORFTQVSDLELFGGPNWGLVAFVFGAALCAESVKNKEMEPLVG 120
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QY 181 GALVTVGAFPAASK 193
Db 181 GALVTVGAFPAASK 193
RESULT 2
088996
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ID 088996 PRELIMINARY; PRT; 193 AA.
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DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Bcl-w (Hypothetical protein).
GN Name=bcl-w;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=99292146; PubMed=10366024; DOI=10.1016/S0306-4522(98)00642-3;
RA Hammer S., Skoglous Y., Lindholm D.;
RT "Differential expression of bcl-w and bcl-x messenger RNA in the
RT developing and adult rat nervous system.";
RL Neuroscience 91:673-684(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22672518; PubMed=12787069;
RA Itoh T., Itoh A., Pleasure D.;
RT "Bcl-2-related protein family gene expression during oligodendroglial
RT differentiation.";
RL J. Neurochem. 85:1500-1512(2003).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubln G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smalins D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF096291; AAC64200.1; -.
DR EMBL; AY185098; AAC64468.1; -.
DR EMBL; BC074021; AAT74021.1; -.
DR HSSP; Q92843; 100L.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
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KW Hypothetical protein.  
SQ SEQUENCE 193 AA; 20820 MW; 36D6742F4529AFB4 CRC64;  
Query Match 99.6%; Score 1005; DB 2; Length 193;  
Best Local Similarity 99.5%; Pred. No. 5.8e-82;  
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPADPLHQAAMRAAGDEFEFRRT 60  
DB 1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPADPLHQAAMRAAGDEFEFRRT 60

QY 61 FSDLAALHTPTPGSAOQRFTQVSDELFOGGPNWGRVAFVFGAALCAESVNMKEPLVG 120  
DB 61 FSDLAALHTPTPGSAOQRFTQVSDELFOGGPNWGRVAFVFGAALCAESVNMKEPLVG 120

QY 121 QVQDMWVAYLETRLDWIHSSGGWAEFTALYGDGALBEARRLREGNWASVRTLGTGAVAL 180  
DB 121 QVQDMWVAYLETRLDWIHSSGGWAEFTALYGDGALBEARRLREGNWASVRTLGTGAVAL 180

QY 181 GALVTVGAFPAASK 193  
DB 181 GALVTVGAFPAASK 193

RESULT 3  
Q7TS60 PRELIMINARY; PRT; 219 AA.  
AC Q7TS60;  
DT 01-OCT-2003 (TReMBLrel. 25, Created)  
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE BCL-WEL.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=22672518; PubMed=12787069;  
RA Itoh T., Itoh A., Pleasure D.;  
RT "Bcl-2-related protein family gene expression during oligodendroglial  
RT differentiation.";  
RL J. Neurochem. 85:1500-1512(2003).  
DR EMBL; AY185100; AAC64470.1; -.  
DR HSSP; Q07817; 1R2D.  
DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; Bcl2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
SQ SEQUENCE 219 AA; 23720 MW; 30E36041BC1DC66F CRC64;

Query Match 99.6%; Score 1005; DB 2; Length 219;  
Best Local Similarity 99.5%; Pred. No. 6.7e-82;  
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPADPLHQAAMRAAGDEFEFRRT 60  
DB 27 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPADPLHQAAMRAAGDEFEFRRT 86

QY 61 FSDLAALHTPTPGSAOQRFTQVSDELFOGGPNWGRVAFVFGAALCAESVNMKEPLVG 120  
DB 87 FSDLAALHTPTPGSAOQRFTQVSDELFOGGPNWGRVAFVFGAALCAESVNMKEPLVG 146

QY 121 QVQDMWVAYLETRLDWIHSSGGWAEFTALYGDGALBEARRLREGNWASVRTLGTGAVAL 180  
DB 147 QVQDMWVAYLETRLDWIHSSGGWAEFTALYGDGALBEARRLREGNWASVRTLGTGAVAL 206

QY 181 GALVTVGAFPAASK 193  
DB 207 GALVTVGAFPAASK 219

RESULT 4  
BCLW\_HUMAN STANDARD; PRT; 193 AA.  
ID BCLW\_HUMAN  
AC Q92843;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Apoptosis regulator Bcl-w (Bcl-2-like 2 protein).  
GN Name=BCL2L2; Synonyms=BCLW, KIAA0271;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96358615; PubMed=8761287;  
RA Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,  
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;  
RT "Bcl-w, a novel member of the bcl-2 family, promotes cell survival.";  
RL Oncogene 13:665-675(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=97191544; PubMed=9039502;  
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,  
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;  
RT "Prediction of the coding sequences of unidentified human genes. VI.  
RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by  
RT analysis of cDNA clones from cell line KG-1 and brain.";  
RL DNA Res. 3:321-329(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.B.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- FUNCTION: Promotes cell survival.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and  
CC in a wide range of tissues, with highest levels in brain, colon,  
CC and salivary gland.  
CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic  
CC function.  
CC -1- SIMILARITY: Belongs to the Bcl-2 family.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; U59747; AAB09055.1; -  
DR EMBL; D87461; BAA19666.2; ALT\_INIT.  
DR EMBL; BC021198; AAH21198.1; -  
DR PDB; 1MK3; NMR; A=2-172.  
DR PDB; 1OOL; NMR; A=1-183.  
DR Genew; HGNC:995; BCL2L2.  
DR H-invDB; HIX0011536; -  
DR MTM; 601931; -  
DR GO; GO:0005737; C:cytoplasm; NAS.  
DR GO; GO:0006916; P:anti-apoptosis; TAS.  
DR GO; GO:0007283; P:spermatogenesis; TAS.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
DR 3D-structure; Apoptosis.  
FT DOMAIN 9 BH4.  
FT DOMAIN 85 104 BH1.  
FT DOMAIN 136 151 BH2.  
SQ SEQUENCE 193 AA; 20774 MW; 3792243A50281761 CRC64;  
  
Query Match 99.1%; Score 1000; DB 1; Length 193;  
Best Local Similarity 99.0%; Pred. No. 1.6e-81;  
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MATPASTPDTRALVADFGVGYKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAALHTVTPGSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVKNKMEPLVG 120  
DB 61 FSDLAALHTVTPGSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVKNKMEPLVG 120  
QY 121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTLGTGAVAL 180  
DB 121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTLGTGAVAL 180  
QY 181 GALVTVGAFPAASK 193  
DB 181 GALVTVGAFPAASK 193  
  
RESULT 5  
Q6A093 PRELIMINARY; PRT; 192 AA.  
AC Q6A093;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE MKIAA0271 protein (Fragment).  
GN Name=MKIAA0271;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,  
RA Saga Y., Saito S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,  
RA Nagase T., Ohara O., Koga H.;  
RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:  
RT IV. The Complete Nucleotide Sequences of 500 Mouse KIAA Homologues  
RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones  
RT Randomly Sampled from Size-Fractionated Libraries";  
RL DNA Res. 11:205-218(2004).  
DR EMBL; AK172925; BAD32203.1; -  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0005515; F:protein binding; IPT.  
DR GO; GO:0006915; P:apoptosis; IDA.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
FT NON TER 1  
SQ SEQUENCE 192 AA; 20763 MW; A56CE4EC51D41F8A CRC64;  
  
Query Match 98.7%; Score 996; DB 2; Length 192;  
Best Local Similarity 100.0%; Pred. No. 3.7e-81;  
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MATPASTPDTRALVADFGVGYKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60  
DB 2 MATPASTPDTRALVADFGVGYKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 61  
QY 61 FSDLAALHTVTPGSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVKNKMEPLVG 120  
DB 62 FSDLAALHTVTPGSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVKNKMEPLVG 121  
QY 121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTLGTGAVAL 180  
DB 122 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTLGTGAVAL 181  
QY 181 GALVTVGAF 190  
DB 182 GALVTVGAF 191  
  
RESULT 6  
Q8CGL4 PRELIMINARY; PRT; 193 AA.  
ID Q8CGL4;  
AC Q8CGL4;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Bcl2-like protein 2.  
GN Name=Bcl2l2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL; TISSUE=Skin;  
RA Su H.-Y., Cheng W.T.K., Chen S.C., Lin C.T., Lien Y.Y., Liu H.J.,  
RA Gilmour R.S.;  
RT "Mouse keratinocytes express c98, a novel gene homologous to bcl-2,  
RT that is stimulated by insulin-like growth factor 1 and prevents  
RT dexamethasone-induced apoptosis.";  
RL Biochim. Biophys. Acta 1676:127-137(2004).  
DR EMBL; AY170344; AA013177.2; -  
DR HSSP; Q92843; 100L.  
DR MGD; MGI:108052; Bcl2l2.



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DR GO; GO:0016021; C:Integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006915; P:apoptosis; IDA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
SQ SEQUENCE 193 AA; 20958 MW; 60D7F9E4DC56DFAB CRC64;

Query Match          95.1%; Score 960; DB 2; Length 193;
Best Local Similarity 95.9%; Pred. No. 6.2e-78;
Matches 185; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MATPASTPDTRALVADFVGKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60
DB 1 MATPASTPDTRALVAVFYVGYLQKQGYVCGAGPEGPAADPLHQAMRAAGDELQTRFRRT 60
QY 61 FSDLAQLHTVPGSAQQRFTQVSDLEFGGPNWGRLLVAFVFGAALCAESVKNKMEPLVG 120
DB 61 FSHLAAQLHTVPGSAQQRFTQVSDLEFGGPNWGRLLVAFVFGAALCAESVKNKMEPLVG 120
QY 121 QVQDMWVAVLETRLADWIIHSSGGWAEFTALYGDGALBEARRLREGNWASVTVLTGAVAL 180
DB 121 QVQDMWVAVLETRLADWIIHSSGGWAEFTALYGDGALBEARRLREGNWASVTVLTGAVAL 180
QY 181 GALVTGAFPAFK 193
DB 181 GALVTGAFPAFK 193
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RESULT 7
Q8CFR2 PRELIMINARY; PRT; 178 AA.
AC Q8CFR2;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Bcl2l2 protein.
GN Name=Bcl2l2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kesteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.B., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC040369; AAH40369.1; -.
DR HGSP; Q92843; 100L.
DR MGD; MGI:108052; Bcl2l2.
DR GO; GO:0016021; C:Integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006915; P:apoptosis; IDA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 178 AA; 19119 MW; E2C3F3F79528E9D7 CRC64;

Query Match          76.3%; Score 770; DB 2; Length 178;
Best Local Similarity 96.7%; Pred. No. 5.9e-61;
Matches 145; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MATPASTPDTRALVADFVGKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60
DB 1 MATPASTPDTRALVADFVGKLRQKGYVCGAGPEGPAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHTVPGSAQQRFTQVSDLEFGGPNWGRLLVAFVFGAALCAESVKNKMEPLVG 120
DB 61 FSDLAQLHTVPGSAQQRFTQVSDLEFGGPNWGRLLVAFVFGAALCAESVKNKMEPLVG 120
QY 121 QVQDMWVAVLETRLADWIIHSSGGWAEFTAL 150
DB 121 QVQDMWVAVLETRLADWIIHSSGGWVRSSQL 150
```

```
RESULT 8
Q9CYW5 PRELIMINARY; PRT; 178 AA.
AC Q9CYW5;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2810435A13 product:Bcl2-like 2, full insert
DE sequence.
GN Name=Bcl2l2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=whole body;
```

RA The PANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630 (2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Kashwagi K.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Harada A.,  
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771 (2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,  
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.,  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK013244; BAB28740.1; -.  
DR HSSP; Q92843; 100L.  
DR MGD; MGI:108052; Bcl2l2.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0006915; P:apoptosis; IDA.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH.  
DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SMO0337; BCL; 1.  
DR SMART; SMO0265; BH4; 1.  
DR PROSITE; PSS0062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PSS0063; BH4\_2; 1.  
SQ SEQUENCE 178 AA; 15147 MW; E2D4C3F79528E9D7 CRC64;  
Query Match 76.3%; Score 770; DB 2; Length 178;  
Best Local Similarity 96.7%; Pred. No. 5.9e-61;  
Matches 145; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MATPASTPDTRALVADVFVGYKLRQKGYCGAGPGEPAADPLHQAMRAAGDEFEFRFRRT 60  
DB 1 MATPASTPDTRALVADVFVGYKLRQKGYCGAGPGEPAADPLHQAMRAAGDEFEFRFRRT 60  
QY 61 FSDLAQLHTVPGSAQORFTQVSDLEFGGPNMGRVAFVFGALCAESVKNEMEPLVG 120  
DB 61 FSDLAQLHTVPGSAQORFTQVSDLEFGGPNMGRVAFVFGALCAESVKNEMEPLVG 120

QY 121 QVQDMVAYLETRLADWTHSSGCGWAEFTAL 150  
DB 121 QVQDMVAYLETRLADWTHSSGCGWVRSSQL 150  
RESULT 9  
Q6GP82 PRELIMINARY; PRT; 188 AA.  
AC Q6GP82;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE MGC80617 protein.  
GN Name=MGC80617;  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603699;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalski U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.,  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative.";  
RL Dev. Dyn. 225:384-391 (2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Klein S., Gerhard D.S.,  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073259; AAH73259.1; -.  
DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH.  
DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SMO0337; BCL; 1.  
DR SMART; SMO0265; BH4; 1.  
DR PROSITE; PSS0062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
SQ SEQUENCE 188 AA; 20441 MW; CB3C1A8C55F16B96 CRC64;  
Query Match 65.0%; Score 655.5; DB 2; Length 188;

Best Local Similarity 69.4%; Pred. No. 1.1e-50;  
Matches 127; Conservative 19; Mismatches 34; Indels 3; Gaps 1;  
QY 11 RALVADPVGYKLRQKGYVCAGPGEGPADPLHQAMRAAGDEFETRFRRTFSDLAQLHV 70  
Db 9 RALVEDFVRYKLCQRLV--PEPAGPASCALHSAMRAAGDEFEEFRQAFFSEISTQIHV 65  
QY 71 TPGSAQQRFTQVSDLEFQGGPNWGRVAFVFGAALCAESVNKEMEPLVGQVQDMWVAYL 130  
Db 66 TPGTAYARFAEVAAGSLFQGGVNWGRIVAFVFGAALCAESVNKEMSPILPRIQDMWVAYL 125  
QY 131 ETRLADWIIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTVLTGAVALGALVTGAF 190  
Db 126 ETNLRGWIGSNGWNGFLLTYGDGAIPEARQRREGNWSLKTVLTGAVALGALMTVGALF 185  
QY 191 ASK 193  
Db 186 ASK 188

RESULT 10

ARI\_XENLA STANDARD; PRT; 228 AA.  
ID ARI\_XENLA  
AC Q91827;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 29-MAR-2004 (Rel. 43, Last annotation update)  
DE Apoptosis regulator R1 (XRL) (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Head;  
RX MEDLINE=95331613; PubMed=7607538; DOI=10.1016/0378-1119(95)00159-4;  
RA Cruz-Reyes J., Tata J.R.;  
RT "Cloning, characterization and expression of two Xenopus bcl-2-like  
cell-survival genes.";  
RL Gene 158:171-179(1995).  
CC -1- FUNCTION: Could be the homolog of mammalian Bcl-W.  
CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).  
CC -1- DEVELOPMENTAL STAGE: Developmental regulation only occurs in the  
brain of mid-metamorphic to post-metamorphic tadpoles and  
adults, where an increase of several fold has been observed.  
CC -1- SIMILARITY: Belongs to the Bcl-2 family.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X82462; CAA57845.1; -.  
DR HSSP; Q07817; IMAZ.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; Bcl2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR Apoptosis; Transmembrane.  
FT NON\_TER 1 1  
FT DOMAIN 120 139 BH1.  
FT DOMAIN 171 186 BH2.  
FT TRANSMEM 207 227 Potential.

SQ SEQUENCE 228 AA; 25068 MW; C499D449A585F8A9 CRC64;  
Query Match  
Best Local Similarity 64.5%; Score 650.5; DB 1; Length 228;  
Matches 126; Conservative 20; Mismatches 35; Indels 3; Gaps 1;  
QY 10 TRALVADPVGYKLRQKGYVCAGPGEGPADPLHQAMRAAGDEFETRFRRTFSDLAQLH 69  
Db 48 SRALVEDLVRYKLCQRLV--PEPSGAASCALHSAMRAAGDEFEEFRQAFFSEISTQIH 104  
QY 70 VTPGSAQQRFTQVSDLEFQGGPNWGRVAFVFGAALCAESVNKEMEPLVGQVQDMWVAY 129  
Db 105 VTPGTAYARFAEVAAGSLFQGGVNWGRIVAFVFGAALCAESVNKEMSPILPRIQDMWVAY 164  
QY 130 LETRLADWIIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTVLTGAVALGALVTGAF 189  
Db 165 LETNLRDWIGSNGWNGFLLTYGDGAIPEARQRREGNWSLKTVLTGAVALGALMTVGAL 224  
QY 190 FASK 193  
Db 225 FASK 228

RESULT 11

Q9MYW4 PRELIMINARY; PRT; 233 AA.  
ID Q9MYW4  
AC Q9MYW4;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Bcl-X.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Knott J.C., Robertson L., James E.R.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY005131; AAF88137.1; -.  
DR HSSP; P53563; 1AF3.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS01260; BH4\_2; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
SQ SEQUENCE 233 AA; 25986 MW; 12F0F30344D53F93 CRC64;  
Query Match  
Best Local Similarity 43.6%; Score 439.5; DB 2; Length 233;  
Matches 94; Conservative 22; Mismatches 57; Indels 51; Gaps 4;  
QY 11 RALVADPVGYKLRQKGYVC-----GAG-----PGECPAA 39  
Db 6 RELVVDPLSYKLSQKGYWSQFSVDEENRTEAPEGTGPEMETPSAINGNPAMHPADSPAV 65  
QY 40 D-----PLHQAMRAAGDEFETRFRRTFSDLAQLHVTGPSAQQRFTQ 81  
Db 66 NGATGHSSSLDAREVITPMTAVKQALREAGDEFELRYRRAFSDLSQLHITPGTAYOSFEQ 125  
QY 82 VSDELFGGPNWGRVAFVFGAALCAESVNKEMEPLVGQVQDMWVAYLETRLADWIIHSS 141

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Db      126 VVNELFRDGVNMGRIVAFSPFGALCVESVDKEMEVLVSRIAMMATYLNHLEPWIQEN 185
QY      142 GGMAEFTALYDGCALBEARLRE--GNWASVRTLVTGAVLGCAL 183
Db      186 GGMWTFVELYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 12
BCLX_CHICK
ID_BCLX_CHICK STANDARD; PRT; 229 AA.
AC Q07816; Q98908;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
GN Name=BCL2L1; Synonyms=BCL-X, BCLX;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=93364977; PubMed=8358789; DOI=10.1016/0092-8674(93)90508-N;
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator of
RT apoptotic cell death."
RL Cell 74:597-608(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN=Hubbard White Mountain; TISSUE=Testis;
RX MEDLINE=97264485; PubMed=9110311;
RX DOI=10.1002/(SICI)1098-2795(199705)47:1<26::AID-MRD4>3.3.CO;2-V;
RA Vilagrasa X., Mezquita C., Mezquita J.;
RT "Differential expression of bcl-2 and bcl-x during chicken
RT spermatogenesis."
RL Mol. Reprod. Dev. 47:26-29(1997).
CC -1- FUNCTION: Dominant regulator of apoptotic cell death. The long
CC form displays cell death repressor activity, whereas the short
CC isoform promotes apoptosis (By similarity).
CC -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC envelope (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q07816-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q07816-2; Sequence=VSP_000514;
CC -1- TISSUE SPECIFICITY: Highest expression in organs with lymphoid
CC development.
CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC function. Intact BH1 and BH2 domains are required for anti-
CC apoptotic activity (By similarity).
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -----
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CC -----
DR EMBL; Z23110; CAA80657.1; -.
DR EMBL; U26645; AAB07677.1; -.
DR PIR; A47537; A47537.
DR HSSP; P53563; 1AF3.
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DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR TIGRfams; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
KW Alternative splicing; Apoptosis; Transmembrane.
FT DOMAIN 4 24 BH4.
FT DOMAIN 82 96 BH3.
FT DOMAIN 125 144 BH1.
FT DOMAIN 176 191 BH2.
FT TRANSMEM 206 223 Potential.
FT VARSPPLIC 185 229 ERFVLYGNNAAEALRKQETFNKLLTGATVAGVLLIGSL
FT LSRK -> VRTALP (in isoform short).
FT /FTID=VSP_000514.
SQ SEQUENCE 229 AA; 25733 MW; A97D3A4D04C0E9DA CRC64;

Query Match 42.9%; Score 432.5; DB 1; Length 229;
Best Local Similarity 41.7%; Pred. No. 1.3e-30;
Matches 95; Conservative 22; Mismatches 62; Indels 49; Gaps 4;

QY 11 RALVADFYGYKLRQKGY-----VCGAGPGECP----- 37
Db 6 RELVIDFVSYKLSQRGHCSLEBEDENRTDTAAEAEMDSVLNGSPSWHPAGHYVNGAT 65
QY 38 -----AADPLHQAMRAAGDEFETRFRRTFSDLAQLHTVPGSAQQRFTQVSDE 85
Db 66 VHRSSLEVHEIVRASDVRLQALRDAGDEFELRYRRAFSDLTSQLHTTPGTAYQSFQVNE 125
QY 86 LFQGGPNWGRLVAFVFFGAALCAESVNKEMEPLVGQDMMVAYLLETRLADWTHSSGWA 145
Db 126 LFHDGVNMGRIVAFSPFGALCVESVDKEMRVLVGRIVSWMTTYLTDLDPWTQENGWE 185
QY 146 EFTALYDGCALBEARLREGNWSVRTLVTGAVLGCALVTGAFASK 193
Db 186 RFVVDLYGNNA--AAELRKQGETFNKLLTGATVAGVLL-LGSLLSRK 229

RESULT 13
Q8SQ42 PRELIMINARY; PRT; 233 AA.
AC Q8SQ42;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Bcl-x1 protein.
GN Name=bcl-x1;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Nagafuchi S., Sano J., Kano R., Hasegawa A.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB080951; BAB85856.2; -.
DR HSSP; Q07817; 1MAZ.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
```



[illegible]

```

CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ001203; CAA04597.1; -.
DR HSSP; Q07817; IMAZ.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR TIGRfams; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
DR Apoptosis; Mitochondrion; Transmembrane.
KW DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.
FT DOMAIN 180 195 BH2.
FT TRANSMEM 210 226 Potential.
SQ SEQUENCE 233 AA; 26061 MW; 18BF6FA0441912B2 CRC64;

Query Match 42.8%; Score 431.5; DB 1; Length 233;
Best Local Similarity 41.8%; Pred. No. 1.6e-30;
Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADFVGYKLRQKGY-----V 28
   ||| ||| ||| |||
Db 6 RELVDFLSYKLSQKGSWSQFTDVEENRTEAEGTSEAEPTSPAINGNPSWHLADSPAV 65

QY 29 CGAGPEGGPAD-----PLHQAMRAAGDEFETRFRRTFSDLAQLHVTFGSAOQRF 80
   || | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 66 NGA-TGHSSSLDAREVIMAAVKKQALREAGDEFELRYRRAFSDLTSQLHTTGTAYQSFE 124

QY 81 QVSDELFOGGPNNGRLVAFVFGAALCAESVKNKMEPLVGQVQDMVAVYLETRLADWHS 140
   || : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 125 QVLNELFRDGVNNGRIVAFSFGALCVESYDKEMQVLVSRIATWMAIYLNHLEPWIQ 184

QY 141 SGWABFTALYGDGALBEBRLRE--GNWASVRTVLTGAVALGAL 183
   : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 185 NGWDTFVELYGNNAAAESRKQGERFNRWFLTGMTLAGVLLGSL 229

RESULT 15
Q9N1A2 PRELIMINARY; PRT; 233 AA.
AC Q9N1A2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Anti-apoptotic regulator Bcl-xl.
GN Name=bcl-xl;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Lee T.L., Cauty J.M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF216205; AAF33212.1; -.

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DR HSSP; Q07817; 1R2D.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; Bcl2\_family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
SQ SEQUENCE 233 AA; 26047 MW; 2FA312818B25E17D CRC64;

Query Match 42.8%; Score 431.5; DB 2; Length 233;  
Best Local Similarity 41.8%; Pred.No.1.6e-30;  
Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADFVGYKLRQKY-----V 28  
Db 6 RELVVDLSTYKLSQKGYSGFTDVEENRTEAPEGTSEAEFTPSAINGNPSWHLADSPAV 65  
QY 29 CGAGPGECPAD-----PLHQAMRAAGDEFETFRFRRTFSDLAQLHVTTPGSAQORFT 80  
Db 66 NGA-TGHSSSLDAREVTPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124  
QY 81 QVSDELFOGGPNWGRVAFVFGAALCAESVNKEMEPVYGQVQDMVAYLETRLADWIHS 140  
Db 125 QYVNELFRDGVNWGRIVAFSFGALCVESVDKEMQVLVSRIATWMTATYLNHDHLEPWIOE 184  
QY 141 SGGWAEFTALYGDALAEARLRE--GNWASVRTVLTGAVALLGAL 183  
Db 185 NGGWDTFVELYGNMAAESRKQGERFNRWFLTGMTLAGVLLGSL 229

Search completed: April 10, 2005, 22:42:54  
Job time : 60 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 10, 2005, 20:12:38 ; Search time 65 Seconds  
(without alignments)  
1148.381 Million cell updates/sec

Title: US-09-925-674B-9  
Perfect score: 1009  
Sequence: 1 MATPASTPDTRALVADFGVY.....LTGAVALGALVTVGAFPAASK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1009	100.0	193	2	AAV05531	Aay05531 Mouse Bcl
2	1005	99.6	193	2	AAW61391	Aaw61391 Rat bcl-y
3	1005	99.6	193	2	AAW97391	Aaw97391 The rat b
4	1000	99.1	192	2	AAW97393	Aaw97393 Protein g
5	1000	99.1	193	2	AAV05530	Aay05530 Human Bcl
6	1000	99.1	193	7	ADD46742	Add46742 Human Pro
7	1000	99.1	193	8	ADP88349	Adp88349 Human Bcl
8	995	98.6	193	2	AAW61392	Aaw61392 Human bcl
9	995	98.6	193	2	AAW97392	Aaw97392 The human
10	993	98.4	193	2	AAW36047	Aaw36047 Human bcl
11	993	98.4	193	2	AAV05532	Aay05532 Human Bcl
12	990	98.1	192	2	AAW97394	Aaw97394 Mammalian
13	967.5	95.9	192	2	AAV05533	Aay05533 Mouse Bcl
14	947	93.9	183	8	ADP88350	Adp88350 Derivativ
15	876	86.8	168	2	AAW36048	Aaw36048 Mouse bcl
16	814.5	80.7	190	5	AAO18223	Aao18223 Human Bcl
17	759	75.2	365	2	AAW59884	Aaw59884 Amino aci
18	759	75.2	365	5	ABG95556	Abg95556 Human nov
19	759	75.2	365	6	ABO34750	Ab034750 Fragment
20	759	75.2	365	7	ADI23411	Adi23411 Novel hum
21	759	75.2	365	8	ADH74413	Adh74413 Human sec
22	757.5	75.1	185	8	ABM84148	Abm84148 Human dia
23	457.5	45.3	179	8	ADH52635	Adh52635 Chinese h
24	448.5	44.4	199	8	ADH52637	Adh52637 Chinese h
25	441.5	43.8	219	8	ADH52639	Adh52639 Chinese h

26	436.5	43.3	219	8	ADH52641	Adh52641 Chinese h
27	436.5	43.3	342	8	ADQ97763	Adq97763 Mouse can
28	432.5	42.9	411	4	AAU00219	Aau00219 Bcl-X1-DT
29	431.5	42.8	233	8	ADQ80679	Adq80679 Porcine a
30	430.5	42.7	237	5	ABG78480	Abg78480 Wild type
31	429.5	42.6	233	8	ADH52633	Adh52633 Chinese h
32	428.5	42.5	233	4	AAB73303	Aab73303 Rat wild-
33	428.5	42.5	233	7	ADE62921	Ad62921 Rat Prote
34	428.5	42.5	233	8	ADQ80678	Adq80678 Mouse ant
35	427.5	42.4	233	2	AAR68887	Aar68887 Human thy
36	427.5	42.4	233	2	AAW05821	Aaw05821 Bcl-XL pr
37	427.5	42.4	233	2	AAW31530	Aaw31530 Human ant
38	427.5	42.4	233	3	AAV69969	Aay69969 Human Bcl
39	427.5	42.4	233	3	AAV83223	Aay83223 Bcl-x pol
40	427.5	42.4	233	4	AAB50538	Aab50538 Human Bcl
41	427.5	42.4	233	4	AAG64262	Aag64262 Human Bcl
42	427.5	42.4	233	4	AAB47515	Aab47515 Protein e
43	427.5	42.4	233	7	ADE62493	Ad62493 Human Pro
44	427.5	42.4	233	7	ABW02410	Abw02410 Human bcl
45	427.5	42.4	233	7	ABW02410	Abw02410 Human bcl

ALIGNMENTS

RESULT 1  
ID AAY05531 standard; protein; 193 AA.  
XX AAY05531;  
AC AAY05531;  
DT 05-JUL-1999 (first entry)  
XX  
XX Mouse Bcl-w protein essential for spermatogenesis.  
DE  
XX Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;  
KW animal model.  
XX  
XX Mus sp.  
OS  
XX  
XX W09913710-Al.  
PN  
XX  
XX 25-MAR-1999.  
PD  
XX  
XX 16-SEP-1998; 98WO-AU000764.  
PF  
XX 16-SEP-1997; 97AU-00009228.  
PR  
XX  
XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
PA  
XX  
XX Cory S, Adams J, Print C, Gibson L, Koentgen F;  
PI  
XX WPI; 1999-243890/20.  
XX N-PSDB; AAX25133.  
DR  
XX  
XX An animal model exhibiting reduced levels of a Bcl-w protein and/or  
PT protein associated with Bcl-w.  
PT  
XX  
XX Claim 2; Page 35; 52pp; English.  
XX  
XX The present sequence is mouse Bcl-w, a pro-survival member of the Bcl-2  
CC family which is widely expressed and which is essential for  
CC spermatogenesis. The invention relates generally to a method of treatment  
CC and to an animal model for the identification of molecules and genetic  
CC sequences useful for inducing or reducing fertility of male animals.  
CC Methods are provided for the treatment of infertility, or for reducing  
CC fertility, by modulating spermatogenesis. An animal model carries a  
CC mutation is at least one allele of the human or murine bcl-w gene (see  
CC AAX25132-35) or in a gene associated with bcl-w. Such animals have  
CC disorganised seminiferous tubules and are substantially infertile, but  
CC possess no other major abnormalities as determined by histological  
CC examination. They can be used to screen for therapeutic molecules  
CC including genetic sequences capable of inducing, enhancing or otherwise

CC facilitating spermatogenesis in animals, or which can induce infertility  
XX  
SQ Sequence 193 AA;

Query Match 100.0%; Score 1009; DB 2; Length 193;  
Best Local Similarity 100.0%; Pred. No. 9.3e-102;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASTPDRALVADFGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASTPDRALVADFGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAQAQLHVTTPGSAQORFTQVSDLEFQGGPNWGRLVAFVFGALCAESVNKEMEPLVG 120  
DB 61 FSDLAQAQLHVTTPGSAQORFTQVSDLEFQGGPNWGRLVAFVFGALCAESVNKEMEPLVG 120  
QY 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLRGNWASVRTVLTGAVAL 180  
DB 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLRGNWASVRTVLTGAVAL 180  
QY 181 GALVTVGAFPAASK 193  
DB 181 GALVTVGAFPAASK 193

RESULT 2  
AAW61391  
ID AAW61391 standard; protein; 193 AA.

AC AAW61391;  
XX  
DT 02-OCT-1998 (first entry)  
XX  
DE Rat bcl-y protein.  
XX  
KM bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.  
XX  
OS Rattus sp.  
XX  
PN US5789201-A.  
XX  
PD 04-AUG-1998.  
XX  
PF 11-FEB-1997; 97US-00798897.  
XX  
PR 23-FEB-1996; 96US-0012201P.  
XX  
PA (COCE-) COCENSYS INC.  
XX  
PI Guastella J;  
XX  
DR WPI; 1998-446079/38.  
DR N-PSDB; AAV28333.  
XX  
PT Nucleic acids encoding B-cell lymphoma-y protein - useful for producing  
PT recombinant protein for use in treating uncontrolled cell growth e.g.  
PT cancers.  
XX  
PS Example; Fig 3A; 27pp; English.  
XX  
CC The mammalian bcl-y protein is a member of the bcl-2 family, components  
CC in the cell death pathway. The bcl-2 family have both apoptotic activity  
CC and the apoptosis blocking activity. bcl-y falls in the apoptosis  
CC activity category. The recombinant protein may be used to prevent  
CC uncontrolled cell growth, either by its direct administration to  
CC recombinant genetic constructs to increase its expression in vivo. Also,  
CC antisense constructs can be used in disorders where prevention of cell  
CC death is desired  
XX  
SQ Sequence 193 AA;

Query Match 99.6%; Score 1005; DB 2; Length 193;  
Best Local Similarity 99.5%; Pred. No. 2.6e-101;

Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDRALVADFGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASTPDRALVADFGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAQAQLHVTTPGSAQORFTQVSDLEFQGGPNWGRLVAFVFGALCAESVNKEMEPLVG 120  
DB 61 FSDLAQAQLHVTTPGSAQORFTQVSDLEFQGGPNWGRLVAFVFGALCAESVNKEMEPLVG 120  
QY 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLRGNWASVRTVLTGAVAL 180  
DB 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLRGNWASVRTVLTGAVAL 180  
QY 181 GALVTVGAFPAASK 193  
DB 181 GALVTVGAFPAASK 193

RESULT 3  
AAW97391  
ID AAW97391 standard; protein; 193 AA.

AC AAW97391;  
XX  
DT 20-MAY-1999 (first entry)  
XX  
DE The rat bcl-y protein.  
XX

KM Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
KM programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
KM head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
KM multiple sclerosis; myocardial infarction; vitally induced cell death;  
KM aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
KM premature cell death; cell death stimulator; prolonged cell life span;  
KM Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.  
XX  
OS Rattus sp.  
XX  
PN US5883229-A.  
XX  
PD 16-MAR-1999.  
XX  
PF 25-NOV-1997; 97US-00978523.  
XX  
PR 23-FEB-1996; 96US-0012201P.  
PR 11-FEB-1997; 97US-00798897.  
XX  
PA (COCE-) COCENSYS INC.  
XX  
PI Guastella J;  
XX  
DR WPI; 1999-214150/18.  
DR N-PSDB; AAX15945.

PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for  
PT modulating programmed cell death.  
XX

PS Disclosure; Col 15-18; 26pp; English.

XX  
CC The present sequence represents rat bcl-y protein (Rbcl-y). The  
CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and  
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in  
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y  
CC proteins may be used to treat conditions associated with a disruption of  
CC the cell death pathway. If they act as cell death inhibitors, they may be  
CC used in therapies to treat subjects suffering from: strokes, head trauma,  
CC Alzheimer's Disease, neural and muscular degenerative diseases  
CC (especially multiple sclerosis), myocardial infarction, vitally induced  
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis  
CC - conditions where cells under go premature cell death as a result of  
CC triggers which may or may not be apparent. They may also be used in this  
CC way to develop cell lines which remain viable in culture for an extended



CC period. In contrast, if they act as cell death stimulators, Bcl-*y* and  
 CC Hbcl-*y* may be used to treat conditions associated with prolonged cell  
 CC life span such as cancer (especially Kaposi's sarcoma and lung cancer)  
 CC and auto/hyperimmune diseases. They may also be used to cause cell death  
 CC in, and hence control, parasites  
 XX  
 SQ Sequence 193 AA;

Query Match 99.6%; Score 1005; DB 2; Length 193;  
 Best Local Similarity 99.5%; Pred. No. 2.6e-101;  
 Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MATPASTPDTRALVADLVGVYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
 DB 1 MATPASTPDTRALVADLVGVYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

OY 61 FSDLAQLHVTTPGSAQQRFTQVSDLELFOGGPNWGRLLVAFVFGAALCAESVKNKEMEPLVG 120  
 DB 61 FSDLAQLHVTTPGSAQQRFTQVSDLELFOGGPNWGRLLVAFVFGAALCAESVKNKEMEPLVG 120

OY 121 QVQDMWVAYLETRLDWIHSSGGWAEFTALYGDALBEARRLREGNWASVRTVLTGAVAL 180  
 DB 121 QVQDMWVAYLETRLDWIHSSGGWAEFTALYGDALBEARRLREGNWASVRTVLTGAVAL 180

OY 181 GALVTGAFPAASK 193  
 DB 181 GALVTGAFPAASK 193

RESULT 4  
 ID AAW97393 standard; protein; 192 AA.  
 AC AAW97393;  
 DT 20-MAY-1999 (first entry)

DE Protein sequence of the specification.  
 XX

KW Rat bcl-*y* protein; Bcl-*y*; human bcl-*y* protein; Hbcl-*y*; bcl-2 homologue;  
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
 KW premature cell death; cell death stimulator; prolonged cell life span;  
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.

OS Unidentified.  
 XX  
 PN US5883229-A.  
 PD 16-MAR-1999.  
 XX  
 PF 25-NOV-1997; 97US-00978523.  
 XX  
 PR 23-FEB-1996; 96US-0012201P.  
 PR 11-FEB-1997; 97US-00798897.  
 XX  
 PA (COCE-) COCENSYS INC.

PI Guastella J;  
 XX  
 DR WPI; 1999-214150/18.

PT Novel bcl-*y* homologues of the rat and human bcl-2 protein - useful for  
 PT modulating programmed cell death.

PS Disclosure; Col 19-20; 26pp; English.

XX The specification describes rat bcl-*y* protein (Bcl-*y*) and human bcl-*y*  
 CC protein (Hbcl-*y*). Bcl-*y* and Hbcl-*y* are homologues of the bcl-2 protein  
 CC thought to be involved in programmed cell death (apoptosis and necrosis).  
 CC Bcl-*y* and Hbcl-*y* proteins may be used to treat conditions associated

CC with a disruption of the cell death pathway. If they act as cell death  
 CC inhibitors, they may be used in therapies to treat subjects suffering  
 CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular  
 CC degenerative diseases (especially multiple sclerosis), myocardial  
 CC infarction, vitally induced cell death, aging, spinal cord injuries and  
 CC amyotrophic lateral sclerosis- conditions where cells under go premature  
 CC cell death as a result of triggers which may or may not be apparent. They  
 CC may also be used in this way to develop cell lines which remain viable in  
 CC culture for an extended period. In contrast, if they act as cell death  
 CC stimulators, Bcl-*y* and Hbcl-*y* may be used to treat conditions associated  
 CC with prolonged cell life span such as cancer (especially Kaposi's sarcoma  
 CC and lung cancer) and auto/hyperimmune diseases. They may also be used to  
 CC cause cell death in, and hence control, parasites  
 XX  
 SQ Sequence 192 AA;

Query Match 99.1%; Score 1000; DB 2; Length 192;  
 Best Local Similarity 99.5%; Pred. No. 8.9e-101;  
 Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 ATPASTPDTRALVADLVGVYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61  
 DB 1 ATPASTPDTRALVADLVGVYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60

OY 62 SDLAQLHVTTPGSAQQRFTQVSDLELFOGGPNWGRLLVAFVFGAALCAESVKNKEMEPLVGQ 121  
 DB 61 SDLAQLHVTTPGSAQQRFTQVSDLELFOGGPNWGRLLVAFVFGAALCAESVKNKEMEPLVGQ 120

OY 122 VQDMWVAYLETRLDWIHSSGGWAEFTALYGDALBEARRLREGNWASVRTVLTGAVALG 181  
 DB 121 VQDMWVAYLETRLDWIHSSGGWAEFTALYGDALBEARRLREGNWASVRTVLTGAVALG 180

OY 182 ALVTGAFPAASK 193  
 DB 181 ALVTGAFPAASK 192

RESULT 5  
 ID AAY05530 standard; protein; 193 AA.  
 AC AAY05530;  
 DT 05-JUL-1999 (first entry)

DE Human Bcl-*w* protein essential for spermatogenesis.  
 XX

KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;  
 KW animal model.

OS Homo sapiens.  
 XX  
 PN WO9913710-A1.  
 XX  
 PD 25-MAR-1999.  
 XX  
 PF 16-SEP-1998; 98WO-AU000764.  
 XX  
 PR 16-SEP-1997; 97AU-00009228.

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

PI Cory S, Adams J, Print C, Gibson L, Koentgen F;  
 XX  
 DR WPI; 1999-243890/20.  
 DR N-PSDB; AAX25132.

PT An animal model exhibiting reduced levels of a Bcl-*w* protein and/or  
 PT protein associated with Bcl-*w*.

PS Claim 2; Page 33; 52pp; English.

XX The present sequence is human Bcl-*w*, a pro-survival member of the Bcl-2

CC family which is widely expressed and which is essential for  
CC spermatogenesis. The invention relates generally to a method of treatment  
CC and to an animal model for the identification of molecules and genetic  
CC sequences useful for inducing or reducing fertility of male animals.  
CC Methods are provided for the treatment of infertility, or for reducing  
CC fertility, by modulating spermatogenesis. An animal model carries a  
CC mutation is at least one allele of the human or murine bcl-w gene (see  
CC AAX25132-35) or in a gene associated with bcl-w. Such animals have  
CC disorganised seminiferous tubules and are substantially infertile, but  
CC possess no other major abnormalities as determined by histological  
CC examination. They can be used to screen for therapeutic molecules  
CC including genetic sequences capable of inducing, enhancing or otherwise  
CC facilitating spermatogenesis in animals, or which can induce infertility  
XX  
SQ Sequence 193 AA;

Query Match 99.1%; Score 1000; DB 2; Length 193;  
Best Local Similarity 99.0%; Pred. No. 9e-101;  
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDTRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
Db 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAQLHVTTPGSAQORFTQVSDLEFQGGPNMGRVAVFVFGAALCAESVKNKEMEPVVG 120  
Db 61 FSDLAQLHVTTPGSAQORFTQVSDLEFQGGPNMGRVAVFVFGAALCAESVKNKEMEPVVG 120  
QY 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALAEARRLREGNMAVSRTVLTGAVAL 180  
Db 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALAEARRLREGNMAVSRTVLTGAVAL 180  
QY 181 GALVTVGAFPAK 193  
Db 181 GALVTVGAFPAK 193

RESULT 6  
ADD46742  
ID ADD46742 standard; protein; 193 AA.

XX AC ADD46742;  
XX  
DT 02-DEC-2004 (revised)  
DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein Q92843, SEQ ID NO 12427.  
XX  
KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
OS Homo sapiens.  
OS Unidentified.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
DR WPI; 2003-268312/26.  
DR GENBANK; Q92843.  
XX

PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.

XX  
PS Example 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (described in Table 3  
CC of the specification) which is differentially expressed during pain.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 193 AA;

Query Match 99.1%; Score 1000; DB 7; Length 193;  
Best Local Similarity 99.0%; Pred. No. 9e-101;  
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDTRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
Db 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAQLHVTTPGSAQORFTQVSDLEFQGGPNMGRVAVFVFGAALCAESVKNKEMEPVVG 120  
Db 61 FSDLAQLHVTTPGSAQORFTQVSDLEFQGGPNMGRVAVFVFGAALCAESVKNKEMEPVVG 120  
QY 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALAEARRLREGNMAVSRTVLTGAVAL 180  
Db 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALAEARRLREGNMAVSRTVLTGAVAL 180  
QY 181 GALVTVGAFPAK 193  
Db 181 GALVTVGAFPAK 193

RESULT 7  
ADP88349  
ID ADP88349 standard; protein; 193 AA.

XX AC ADP88349;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Human Bcl-w protein.  
XX  
KW Bcl-w; human; protein structure; protein co-ordinate data.  
XX  
OS Homo sapiens.  
XX  
PN WO2004050697-A1.  
XX  
PD 17-JUN-2004.

XX 03-DEC-2003; 2003WO-AU001624.  
 PF 03-DEC-2002; 2002AU-00953259.  
 PR (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
 PA Hinds MG, Huang DCS, Day CL;  
 PI WPI; 2004-487529/46.  
 DR  
 XX  
 PT Solution useful for identifying or selecting agents that are capable of  
 PT inhibiting biological activity of Bcl-w, comprises molecule that has Bcl-  
 PT w active site defined by specific structure coordinates of Bcl-w amino  
 PT acid residues.  
 PS  
 XX Disclosure; Page 804-805; 810pp; English.  
 CC The present invention relates to a solution comprising a molecule or  
 CC molecular complex that comprises at least a fragment of Bcl-w. Also  
 CC disclosed is the structure of Bcl-w, in the form of protein coordinate  
 CC data. The solution is useful for identifying, selecting or designing  
 CC agents that are capable of inhibiting or potentiating one or more  
 CC biological activity of Bcl-w, and in solving the structures of other  
 CC proteins with similar structure. It is also useful for characterizing the  
 CC three-dimensional structure of the Bcl-w molecule, molecular complex or  
 CC its derivative. The present sequence is the human Bcl-w protein.  
 XX  
 SQ Sequence 193 AA;

Query Match 99.1%; Score 1000; DB 8; Length 193;  
 Best Local Similarity 99.0%; Pred. No. 9e-101;  
 Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 MATPASTPTTRALVADFGVGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRT 60  
 DB 1 MATPASAPDTRALVADFGVGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRT 60  
 OY 61 FSDLAQLHVTTPGSAQQRFTQVSDELFGGPNWGRLLVAFVFGAALCAESVNKEMEPLVG 120  
 DB 61 FSDLAQLHVTTPGSAQQRFTQVSDELFGGPNWGRLLVAFVFGAALCAESVNKEMEPLVG 120  
 OY 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNMAVSVRTLGAVAL 180  
 DB 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNMAVSVRTLGAVAL 180  
 OY 181 GALVTGAFPAK 193  
 DB 181 GALVTGAFPAK 193

RESULT 8  
 AAW61392  
 ID AAW61392 standard; protein; 193 AA.  
 XX  
 AC AAW61392;  
 XX  
 DT 02-OCT-1998 (first entry)  
 XX  
 DE Human bcl-y protein.  
 KW bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5789201-A.  
 XX  
 PD 04-AUG-1998.  
 XX  
 PF 11-FEB-1997; 97US-00798897.  
 XX  
 PR 23-FEB-1996; 96US-0012201P.  
 XX

PA (COCE-) COCENSYS INC.  
 XX  
 PI Guastella J;  
 XX  
 DR WPI; 1998-446079/38.  
 DR N-PSDB; AAV28334.  
 XX  
 PT Nucleic acids encoding B-cell lymphoma-y protein - useful for producing  
 PT recombinant protein for use in treating uncontrolled cell growth e.g.  
 PT cancers.  
 PS  
 XX Example; Column 17/18; 27pp; English.  
 CC The mammalian bcl-y protein is a member of the bcl-2 family, components  
 CC in the cell death pathway. The bcl-2 family have both apoptotic activity  
 CC and the apoptosis blocking activity. bcl-y falls in the apoptosis  
 CC activity category. The recombinant protein may be used to prevent  
 CC uncontrolled cell growth, either by its direct administration to  
 CC recombinant genetic constructs to increase its expression in vivo. Also,  
 CC antisense constructs can be used in disorders where prevention of cell  
 CC death is desired  
 XX  
 SQ Sequence 193 AA;

Query Match 98.6%; Score 995; DB 2; Length 193;  
 Best Local Similarity 98.4%; Pred. No. 3.2e-100;  
 Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 MATPASTPTTRALVADFGVGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRT 60  
 DB 1 MATPASAPDTRALVEDFGVGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEFETRFRRT 60  
 OY 61 FSDLAQLHVTTPGSAQQRFTQVSDELFGGPNWGRLLVAFVFGAALCAESVNKEMEPLVG 120  
 DB 61 FSDLAQLHVTTPGSAQQRFTQVSDELFGGPNWGRLLVAFVFGAALCAESVNKEMEPLVG 120  
 OY 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNMAVSVRTLGAVAL 180  
 DB 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNMAVSVRTLGAVAL 180  
 OY 181 GALVTGAFPAK 193  
 DB 181 GALVTGAFPAK 193

RESULT 9  
 AAW97392  
 ID AAW97392 standard; protein; 193 AA.  
 XX  
 AC AAW97392;  
 XX  
 DT 20-MAY-1999 (first entry)  
 XX  
 DE The human bcl-y protein.  
 KW Rat bcl-y protein; Bcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
 KW premature cell death; cell death stimulator; prolonged cell life span;  
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5883229-A.  
 XX  
 PD 16-MAR-1999.  
 XX  
 PF 25-NOV-1997; 97US-00978523.  
 XX  
 PR 23-FEB-1996; 96US-0012201P.  
 PR 11-FEB-1997; 97US-00798897.  
 XX

XX PA (COCE-) COCENSYS INC.  
XX PI Guastella J;  
XX DR WPI; 1999-214150/18.  
XX DR N-PSDB; AAX15946.  
XX  
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for  
PT modulating programmed cell death.  
XX  
PS Claim 1; Col 17-18; 26pp; English.  
XX  
CC The present sequence represents human bcl-y protein (Hbcl-y). The  
CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-  
CC y are homologues of the bcl-2 protein thought to be involved in  
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y  
CC proteins may be used to treat conditions associated with a disruption of  
CC the cell death pathway. If they act as cell death inhibitors, they may be  
CC used in therapies to treat subjects suffering from: strokes, head trauma,  
CC Alzheimer's Disease, neural and muscular degenerative diseases  
CC (especially multiple sclerosis), myocardial infarction, vitally induced  
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis  
CC - conditions where cells under go premature cell death as a result of  
CC triggers which may or may not be apparent. They may also be used in this  
CC way to develop cell lines which remain viable in culture for an extended  
CC period. In contrast, if they act as cell death stimulators, Rbcl-y and  
CC Hbcl-y may be used to treat conditions associated with prolonged cell  
CC life span such as cancer (especially Kaposi's sarcoma and lung cancer)  
CC and auto/hyperimmune diseases. They may also be used to cause cell death  
CC in, and hence control, parasites  
XX  
SQ Sequence 193 AA;

Query Match 98.6%; Score 995; DB 2; Length 193;  
Best Local Similarity 98.4%; Pred. No. 3.2e-100;  
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MATPASTPDTRALVADFGVGYKLRQKGYVCGAGPGEGPADPLHQAMRAAGDEFETRFRRT 60  
Db 1 MATPASAPDTRALVEDFVGKLRQKGYVCGAGPGEGPADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAQLHVTGPSAQORFTQVSDLEFQGGPNWGRVAFVFGAALCAESVNKEMEPLVG 120  
Db 61 FSDLAQLHVTGPSAQORFTQVSDLEFQGGPNWGRVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQDMWVAYLETRLADWIHSSGGMAEFTALYGDALBEARRLRGNWASVRTVLTGAVAL 180  
Db 121 QVQEMWVAYLETRLADWIHSSGGMAEFTALYGDALBEARRLRGNWASVRTVLTGAVAL 180  
QY 181 GALVTVGAFPAK 193  
Db 181 GALVTVGAFPAK 193

RESULT 10  
AAW36047  
ID AAW36047 standard; protein, 193 AA.  
XX  
AC AAW36047;  
XX  
DT 22-APR-1998 (first entry)  
XX  
DE Human bcl-w protein.  
XX  
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
KM diagnosis; degenerative disease.  
XX  
OS Homo sapiens.  
XX  
PN WO9735971-A1.  
XX  
PD 02-OCT-1997.

XX  
PF -27-MAR-1997; 97WO-AU000199.  
XX  
PR 27-MAR-1996; 96AU-00008965.  
XX  
PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX  
PI Cory S, Adams JM, Gibson LM, Holmgren SP;  
XX  
DR WPI; 1997-489635/45.  
DR N-PSDB; AAT96577.  
XX  
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or  
PT inhibit cell survival, e.g. for treatment of cancer and degenerative  
PT diseases.  
XX  
PS Claim 6; Page 48; 86pp; English.  
XX  
CC This sequence represents a novel human protein, bcl-w, encoded by the bcl  
CC -2 gene family and extracted from an adult brain library. This gene  
CC promotes cell survival, so its modulation is useful in treatment of  
CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,  
CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,  
CC ischaemia, human immunodeficiency virus infection or in cell transplants.  
CC Up-regulation of the gene can also be used to modify cell lines cultured  
CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas  
CC and to increase survival of primary explants during genetic modification.  
CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,  
CC antibody production or screening of potential modulators  
XX  
SQ Sequence 193 AA;

Query Match 98.4%; Score 993; DB 2; Length 193;  
Best Local Similarity 97.9%; Pred. No. 5.3e-100;  
Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MATPASTPDTRALVADFGVGYKLRQKGYVCGAGPGEGPADPLHQAMRAAGDEFETRFRRT 60  
Db 1 MATPASAPDTRALVEDFVGKLRQKGYVCGAGPGEGPADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAQLHVTGPSAQORFTQVSDLEFQGGPNWGRVAFVFGAALCAESVNKEMEPLVG 120  
Db 61 FSDLAQLHVTGPSAQORFTQVSDLEFQGGPNWGRVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQDMWVAYLETRLADWIHSSGGMAEFTALYGDALBEARRLRGNWASVRTVLTGAVAL 180  
Db 121 QVQEMWVAYLETRLADWIHSSGGMAEFTALYGDALBEARRLRGNWASVRTVLTGAVAL 180  
QY 181 GALVTVGAFPAK 193  
Db 181 GALVTVGAFPAK 193

RESULT 11  
AAY05532  
ID AAY05532 standard; protein, 193 AA.  
XX  
AC AAY05532;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Human Bcl-w protein essential for spermatogenesis.  
XX  
KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;  
KM animal model.  
XX  
OS Homo sapiens.  
XX  
PN WO9913710-A1.  
XX  
PD 25-MAR-1999.  
XX  
PF 16-SEP-1998; 98WO-AU000764.



XX 16-SEP-1997; 97AU-00009228.  
 PR (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
 XX  
 PA Cory S, Adams J, Print C, Gibson L, Koentgen F,  
 PI  
 XX WPI; 1999-243890/20.  
 DR N-PSDB; AAX25134.  
 XX  
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
 PT protein associated with Bcl-w.  
 XX  
 PS Disclosure; Page 37; 52pp; English.  
 PS  
 XX The present sequence is described of a derivative of human Bcl-w (see  
 CC also AAY05530), a pro-survival member of the Bcl-2 family that is widely  
 CC expressed and which is essential for spermatogenesis. The invention  
 CC relates generally to a method of treatment and to an animal model for the  
 CC identification of molecules and genetic sequences useful for inducing or  
 CC reducing fertility of male animals. Methods are provided for the  
 CC treatment of infertility, or for reducing fertility, by modulating  
 CC spermatogenesis. An animal model carries a mutation is at least one  
 CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene  
 CC associated with bcl-w. Such animals have disorganised seminiferous tubules  
 CC and are substantially infertile, but possess no other major abnormalities  
 CC as determined by histological examination. They can be used to screen for  
 CC therapeutic molecules including genetic sequences capable of inducing,  
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which  
 CC can induce infertility  
 CC  
 XX Sequence 193 AA;  
 SQ  
 QY Query Match 98.4%; Score 993; DB 2; Length 193;  
 Best Local Similarity 97.9%; Pred. No. 5.3e-100;  
 Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Db 1 MATPASTPDTRALVADVFVGYKLRQKGVCAGPGEPAADPLHQAMRAAGDEFFETRRRT 60  
 1 MATPASAPDTRALVADVFVGYKLRQKGVCAGPGEPAADPLHQAMRAAGDEFFETRRRT 60  
 QY 61 FSDLAQLHVTPEGSAQQRFTQVSDLEFQGGPNWGRVAFVFGAALCAESYNKEMEPLVG 120  
 61 FSDLAQLHVTPEGSAQQRFTQVSDLEFQGGPNWGRVAFVFGAALCAESYNKEMEPLVG 120  
 Db 121 QVQDMWVAYLETRLDWIHSSGWAFFALYGDGALBEARRLREGNWSVTVLTGAVAL 180  
 121 QVQDMWVAYLETRLDWIHSSGWAFFALYGDGALBEARRLREGNWSVTVLTGAVAL 180  
 Db 121 QVQDMWVAYLETRLDWIHSSGWAFFALYGDGALBEARRLREGNWSVTVLTGAVAL 180  
 121 QVQDMWVAYLETRLDWIHSSGWAFFALYGDGALBEARRLREGNWSVTVLTGAVAL 180  
 QY 181 GALVTGAFPAASK 193  
 181 GALVTGAFPAASK 193  
 Db 181 GALVTGAFPAASK 193  
 181 GALVTGAFPAASK 193  
 RESULT 12  
 AAW97394  
 ID AAW97394 standard; protein; 192 AA.  
 XX  
 AC AAW97394;  
 XX  
 DT 20-MAY-1999 (first entry)  
 XX  
 DE Mammalian bcl-y protein.  
 XX  
 KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
 KW premature cell death; cell death stimulator; prolonged cell life span;  
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.  
 XX  
 OS Mammalia.

XX US5883229-A.  
 PN  
 XX 16-MAR-1999.  
 PD  
 XX 25-NOV-1997; 97US-00978523.  
 PF  
 XX 23-FEB-1996; 96US-0012201P.  
 PR 11-FEB-1997; 97US-00798897.  
 XX  
 PA (COCE-) COCENSYS INC.  
 XX  
 PI Guastella J;  
 PI  
 XX WPI; 1999-214150/18.  
 DR  
 XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful for  
 PT modulating programmed cell death.  
 PT  
 XX Claim 2; Col 19-22; 26pp; English.  
 PS  
 XX The present sequence represents a mammalian bcl-1 protein. The  
 CC specification describes rat bcl-y protein (Rbcl-y) and human bcl-y  
 CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein  
 CC thought to be involved in programmed cell death (apoptosis and necrosis).  
 CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated  
 CC with a disruption of the cell death pathway. If they act as cell death  
 CC inhibitors, they may be used in therapies to treat subjects suffering  
 CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular  
 CC degenerative diseases (especially multiple sclerosis), myocardial  
 CC infarction, vitally induced cell death, aging, spinal cord injuries and  
 CC amyotrophic lateral sclerosis- conditions where cells under go premature  
 CC cell death as a result of triggers which may or may not be apparent. They  
 CC may also be used in this way to develop cell lines which remain viable in  
 CC culture for an extended period. In contrast, if they act as cell death  
 CC stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated  
 CC with prolonged cell life span such as cancer (especially Kaposi's sarcoma  
 CC and lung cancer) and auto/hyperimmune diseases. They may also be used to  
 CC cause cell death in, and hence control, parasites  
 CC  
 XX Sequence 192 AA;  
 SQ  
 QY Query Match 98.1%; Score 990; DB 2; Length 192;  
 Best Local Similarity 98.4%; Pred. No. 1.1e-99;  
 Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Db 2 ATPASTPDTRALVADVFVGYKLRQKGVCAGPGEPAADPLHQAMRAAGDEFFETRRRTF 61  
 1 ATPASAPDTRALVEDVFVGYKLRQKGVCAGPGEPAADPLHQAMRAAGDEFFETRRRTF 60  
 QY 62 SDLAQLHVTPEGSAQQRFTQVSDLEFQGGPNWGRVAFVFGAALCAESYNKEMEPLVGQ 121  
 61 SDLAQLHVTPEGSAQQRFTQVSDLEFQGGPNWGRVAFVFGAALCAESYNKEMEPLVGQ 120  
 Db 122 VQDMWVAYLETRLDWIHSSGWAFFALYGDGALBEARRLREGNWSVTVLTGAVALG 181  
 121 VQDMWVAYLETRLDWIHSSGWAFFALYGDGALBEARRLREGNWSVTVLTGAVALG 180  
 QY 182 ALVTGAFPAASK 193  
 182 ALVTGAFPAASK 193  
 Db 181 ALVTGAFPAASK 192  
 181 ALVTGAFPAASK 192  
 RESULT 13  
 AAY05533  
 ID AAY05533 standard; protein; 192 AA.  
 XX  
 AC AAY05533;  
 XX  
 DT 05-JUL-1999 (first entry)  
 XX  
 DE Mouse Bcl-w protein derivative.  
 XX

KM Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;  
KW animal model.

OS Mus sp.

PN WO9913710-A1.

PD 25-MAR-1999.

PF 16-SEP-1998; 98WO-AU000764.

PR 16-SEP-1997; 97AU-00009228.

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

PI Cory S, Adams J, Print C, Gibson L, Koentgen F;

DR WPI; 1999-243890/20.

DR N-PSDB; AAX25135.

PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
PT protein associated with Bcl-w.

PS Disclosure; Page 39; 52pp; English.

CC The present sequence is described of a derivative of mouse Bcl-w (see  
CC also AAY05531), a pro-survival member of the Bcl-2 family that is widely  
CC expressed and which is essential for spermatogenesis. The derivative  
CC lacks the 24 N-terminal amino acids of Bcl-w. The invention relates  
CC generally to a method of treatment and to an animal model for the  
CC identification of molecules and genetic sequences useful for inducing or  
CC reducing fertility of male animals. Methods are provided for the  
CC treatment of infertility, or for reducing fertility, by modulating  
CC spermatogenesis. An animal model carries a mutation is at least one  
CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene  
CC associated with bcl-w. Such animals have disorganised seminiferous tubules  
CC and are substantially infertile, but possess no other major abnormalities  
CC as determined by histological examination. They can be used to screen for  
CC therapeutic molecules including genetic sequences capable of inducing,  
CC enhancing or otherwise facilitating spermatogenesis in animals, or which  
CC can induce infertility  
XX  
SQ Sequence 192 AA;

Query Match Best Local Similarity 95.9%; Score 967.5; DB 2; Length 192;  
Matches 185; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 MATPASTPDRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MPTPASTPDRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAALQHLVTPGSAQQRFTQVSDELFOGGPNNWGRVAFVFGAALCAESVNKEMEPLVG 120  
DB 61 FSDLAALQHLVTPGSAQQRFTQVSDELFOGGPNNWGRVAFVFGAALCAESVNKEMEPLVG 120  
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DB 121 QVQDMWVAVYLETRLADWIHSSGWAFFETALYGDGALLEBARRLREGNWSVRTVLTGAVAL 180  
QY 181 GALVTVGAFPAASK 193  
DB 180 GALVTVGAFPAASK 192

RESULT 14  
ADP88350  
ID ADP88350 standard; protein; 183 AA.  
XX  
AC ADP88350;  
XX  
DT 09-SEP-2004 (first entry)  
XX

DE Derivative of human Bcl-w protein.

XX Bcl-w; human; protein structure; protein co-ordinate data; mutant;  
KW mutein.

OS Homo sapiens.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 128 /note= "wild-type Ala substituted by Glu"

PN WO2004050697-A1.

PD 17-JUN-2004.

PF 03-DEC-2003; 2003WO-AU001624.

PR 03-DEC-2002; 2002AU-00953259.

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

PI Hinds MG, Huang DCS, Day CL;

DR WPI; 2004-487529/46.

PT Solution useful for identifying or selecting agents that are capable of  
PT inhibiting biological activity of Bcl-w, comprises molecule that has Bcl-  
PT w active site defined by specific structure coordinates of Bcl-w amino  
PT acid residues.

PS Claim 16; Page 805-806; 810pp; English.

XX The present invention relates to a solution comprising a molecule or  
XX molecular complex that comprises at least a fragment of Bcl-w. Also  
XX disclosed is the structure of Bcl-w, in the form of protein coordinate  
XX data. The solution is useful for identifying, selecting or designing  
XX agents that are capable of inhibiting or potentiating one or more  
XX biological activity of Bcl-w, and in solving the structures of other  
XX proteins with similar structure. It is also useful for characterizing the  
XX three-dimensional structure of the Bcl-w molecule, molecular complex or  
XX its derivative. The present sequence is a derivative of the human Bcl-w  
XX protein.

SQ Sequence 183 AA;

Query Match Best Local Similarity 93.9%; Score 947; DB 8; Length 183;  
Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASTPDRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASAPDRALVADFGVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAALQHLVTPGSAQQRFTQVSDELFOGGPNNWGRVAFVFGAALCAESVNKEMEPLVG 120  
DB 61 FSDLAALQHLVTPGSAQQRFTQVSDELFOGGPNNWGRVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQDMWVAVYLETRLADWIHSSGWAFFETALYGDGALLEBARRLREGNWSVRTVLTGAVAL 180  
DB 121 QVQDMWVAVYLETRLADWIHSSGWAFFETALYGDGALLEBARRLREGNWSVRTVLTGAVAL 180  
QY 181 GAL 183  
DB 181 GAL 183

RESULT 15  
AAW36048  
ID AAW36048 standard; protein; 168 AA.  
XX  
AC AAW36048;  
XX



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2005, 22:43:04 ; Search time 227.5 Seconds  
(without alignments)  
281.650 Million cell updates/sec

Title: US-09-925-674B-9

Perfect score: 1009

Sequence: 1 MATPASTPTDTRALVADFGVY.....LTGAVALGALVTGAFPAASK 193

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:\*
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  - 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1006	99.7	193	9	US-09-925-674A-9 Sequence 9, Appl1
2	1000	99.1	193	9	US-09-925-674A-7 Sequence 7, Appl1
3	1000	99.1	193	16	US-10-450-366-6 Sequence 6, Appl1
4	759	75.2	365	10	US-09-809-391-696 Sequence 696, App
5	759	75.2	365	10	US-09-882-171-696 Sequence 696, App
6	759	75.2	365	15	US-10-164-861-696 Sequence 696, App
7	631.5	62.6	228	16	US-10-659-705-2 Sequence 2, Appl1
8	457.5	45.3	179	15	US-10-402-017-6 Sequence 6, Appl1
9	448.5	44.4	199	15	US-10-402-017-8 Sequence 8, Appl1
10	441.5	43.8	219	15	US-10-402-017-10 Sequence 10, Appl1
11	436.5	43.3	219	15	US-10-402-017-12 Sequence 12, Appl1
12	432.5	42.9	229	16	US-10-659-705-7 Sequence 7, Appl1
13	432.5	42.9	411	16	US-10-792-517-2 Sequence 2, Appl1

14	429.5	42.6	233	15	US-10-402-017-4	Sequence 4, Appl1
15	427.5	42.4	233	9	US-09-734-846-2	Sequence 2, Appl1
16	427.5	42.4	233	9	US-09-952-278-6	Sequence 6, Appl1
17	427.5	42.4	233	14	US-10-101-482-14	Sequence 14, Appl1
18	427.5	42.4	233	14	US-10-072-830-4	Sequence 4, Appl1
19	427.5	42.4	233	14	US-10-169-223-10	Sequence 10, Appl1
20	427.5	42.4	233	14	US-10-302-262-2	Sequence 2, Appl1
21	427.5	42.4	233	15	US-10-116-275-171	Sequence 171, App
22	427.5	42.4	233	16	US-10-450-366-5	Sequence 5, Appl1
23	427.5	42.4	233	16	US-10-659-705-8	Sequence 8, Appl1
24	415.5	41.2	239	15	US-10-148-953A-3	Sequence 3, Appl1
25	414.5	41.1	152	14	US-10-158-769-2	Sequence 3, Appl1
26	414.5	41.1	233	16	US-10-659-705-3	Sequence 2, Appl1
27	412	40.8	236	13	US-10-087-192-1953	Sequence 1953, Ap
28	411.5	40.8	239	14	US-10-277-693A-10	Sequence 10, Appl
29	411.5	40.8	239	15	US-10-003-632C-10	Sequence 10, Appl
30	411.5	40.8	239	15	US-10-003-632C-13	Sequence 13, Appl
31	409.5	40.6	239	8	US-08-726-211-5	Sequence 5, Appl1
32	409.5	40.6	239	10	US-09-993-420A-8	Sequence 8, Appl1
33	409.5	40.6	239	14	US-10-101-482-12	Sequence 12, Appl
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36	409.5	40.6	239	14	US-10-053-645A-21	Sequence 21, Appl
37	409.5	40.6	239	15	US-10-387-961A-5	Sequence 5, Appl1
38	409.5	40.6	239	15	US-10-003-632C-1	Sequence 1, Appl1
39	409.5	40.6	239	15	US-10-003-632C-3	Sequence 3, Appl1
40	409.5	40.6	239	15	US-10-148-953A-1	Sequence 1, Appl1
41	409.5	40.6	239	15	US-10-148-953A-2	Sequence 2, Appl1
42	409.5	40.6	239	15	US-10-297-321-2	Sequence 2, Appl1
43	409.5	40.6	239	16	US-10-450-366-4	Sequence 4, Appl1
44	409.5	40.6	239	16	US-10-770-668-16	Sequence 16, Appl
45	409.5	40.6	485	16	US-10-792-517-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1									
US-09-925-674A-9									
; Sequence 9, Application US/09925674A									
; Patent No. US20020119943A1									
; GENERAL INFORMATION:									
; APPLICANT: AMRAD Operations Pty Ltd									
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2									
; FILE REFERENCE: 11686a									
; CURRENT APPLICATION NUMBER: US/09/925,674A									
; CURRENT FILING DATE: 2001-08-09									
; PRIOR APPLICATION NUMBER: 09/925,674									
; PRIOR FILING DATE: 2001-08-09									
; PRIOR APPLICATION NUMBER: PN8965									
; NUMBER OF SEQ ID NOS: 9									
; SOFTWARE: PatentIn Ver. 2.1									
; SEQ ID NO 9									
; LENGTH: 193									
; TYPE: PRT									
; ORGANISM: Mouse									
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Matches 192; Conservative 1; Mismatches 0; Indels 0; Gaps 0;									
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DB	1	MATPASTPTDTRALVADFGVYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT	60						
QY	61	FSDLAQLHTVTPGSAQORFTQVSDDELFGGPNWGRLVAFVFGAALCAESVNKEMEPLVG	120						
DB	61	FSDLAQLHTVTPGSAQORFTQVSDDELFGGPNWGRLVAFVFGAALCAESVNKEMEPLVG	120						
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Db 181 GALVTYGAFFASK 193

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US-09-925-674A-7  
; Sequence 7, Application US/09925674A  
; Patent No. US20020119943A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
; FILE REFERENCE: 11686a  
; CURRENT APPLICATION NUMBER: US/09/925,674A  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/925,674  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: PN8965  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-09-925-674A-7

Query Match 99.1%; Score 1000; DB 9; Length 193;  
Best Local Similarity 99.0%; Pred. No. 5.2e-96;  
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
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Db 61 FSDLAQQLHVTTPGSAQQRFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARLRREGNWSVRTVLTGAVAL 180  
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RESULT 3  
US-10-450-366-6  
; Sequence 6, Application US/10450366  
; Publication No. US20040115667A1  
; GENERAL INFORMATION:  
; APPLICANT: Tschopp, Jorg  
; APPLICANT: Hoffmann, Kay  
; TITLE OF INVENTION: DNA-Sequences, Which Code For An Apoptosis Signal Transduction Pr  
; FILE REFERENCE: 11436\*3  
; CURRENT APPLICATION NUMBER: US/10/450,366  
; PRIOR FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: PCT/EP01/14597  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: DE 100 61 766.2  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: DE 101 00 280.7  
; PRIOR FILING DATE: 2001-01-04  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentln version 3.1  
; SEQ ID NO 6  
; LENGTH: 193

; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human Bcl-W  
US-10-450-366-6

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Best Local Similarity 99.0%; Pred. No. 5.2e-96;  
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Db 61 FSDLAQQLHVTTPGSAQQRFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARLRREGNWSVRTVLTGAVAL 180  
Db 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALBEARLRREGNWSVRTVLTGAVAL 180  
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RESULT 4  
US-09-809-391-696  
; Sequence 696, Application US/09809391  
; Publication No. US20030049618A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: PZ002P2  
; CURRENT APPLICATION NUMBER: US/09/809,391  
; PRIOR FILING DATE: 2001-03-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 696  
; LENGTH: 365  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-809-391-696

Query Match 75.2%; Score 759; DB 10; Length 365;  
Best Local Similarity 98.6%; Pred. No. 1.7e-70;  
Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 61 FSDLAQQLHVTTPGSAQQRFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
Db 61 FSDLAQQLHVTTPGSAQQRFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
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Db 121 QVQDMWVAYLETRLADWIHSSGGW 144

RESULT 5  
US-09-882-171-696  
; Sequence 696, Application US/09882171  
; Publication No. US20030175858A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: PZ002P2  
; CURRENT APPLICATION NUMBER: US/09/882,171  
; PRIOR FILING DATE: 2001-06-18



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; PRIOR APPLICATION NUMBER: 60/047,586
; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,594
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,589
; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-04-11
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; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1997-08-22
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; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

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Query Match 75.2%; Score 759; DB 10; Length 365;  
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Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 61 FSDLAQLHTVPGSAQORFTQVSDLEFQGGPNWGRIVAFVFGAALCAESVNKMEPLVG 120
Db 61 FSDLAQLHTVPGSAQORFTQVSDLEFQGGPNWGRIVAFVFGAALCAESVNKMEPLVG 120
QY 121 QVQDMWVAYLETRLADWIHSSGGW 144
Db 121 QVQDMWVAYLETRLADWIHSSGGW 144

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RESULT 6  
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; Sequence 696, Application US/10164861  
; Publication No. US20030225248A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: PZ002p1  
; CURRENT APPLICATION NUMBER: US/10/164,861

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; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 696
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-164-861-696

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Best Local Similarity 98.6%; Pred. No. 1.7e-70;  
Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MATPASTPDRALVADFGYKLRQKGYVCGAGPGEPAADPLHQAAMRAAGDEFETRFRRT 60
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QY 61 FSDLAQLHTVPGSAQORFTQVSDLEFQGGPNWGRIVAFVFGAALCAESVNKMEPLVG 120
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Db 121 QVQDMWVAYLETRLADWIHSSGGW 144

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RESULT 7  
US-10-659-705-2  
; Sequence 2, Application US/10659705  
; Publication No. US20040117867A1  
; GENERAL INFORMATION:  
; APPLICANT: Look, A. Thomas  
; APPLICANT: Langenau, David M.  
; TITLE OF INVENTION: Transgenic Cancer Models in Fish  
; FILE REFERENCE: 112706.123  
; CURRENT APPLICATION NUMBER: US/10/659,705  
; PRIOR FILING DATE: 2003-09-11  
; PRIOR APPLICATION NUMBER: US 60/409,585  
; PRIOR FILING DATE: 2002-09-11  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: BCL2 proteins  
; US-10-659-705-2

Query Match 62.6%; Score 631.5; DB 16; Length 228;  
Best Local Similarity 67.4%; Pred. No. 1.9e-57;  
Matches 124; Conservative 20; Mismatches 37; Indels 3; Gaps 1;

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QY 70 VTPGSAQORFTQVSDLEFQGGPNWGRIVAFVFGAALCAESVNKMEPLVGQVQDMWVAY 129
Db 105 VTPGTAYARFAVAAGSLFQGGVNWGRIVAFVFGAALCAESVNKMEPLVRIQDMWVAY 164
QY 130 LETRLADWIHSSGGWAEFTALYGDGLAEARRLREGNWSAVFTLVGTGAVAGALVTGAF 189
Db 165 LETNLDRLWQSGNGWNGFLTLYGDGLAEARRLREGNWSAVFTLVGTGAVAGALVTGAF 224
QY 190 FASK 193
Db 225 FASK 228

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del26-83)
US-10-402-017-12

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Query Match	43.3%;	Score 436.5;	DB 15;	Length 219;
Best Local Similarity	44.1%;	Pred. No. 4.1e-37;		
Matches 93;	Conservative 22;	Mismatches 57;	T-3-1	20

```

QY      11 RALVADFGYKLRQKGY-----VCGAGPGEGBPAD-- 40
      | | | | | : | | | | |
Db      6 RELVVDLFSYKLSQKGYSWSQFSDVEENRTAPEGTESERAAAAVNGA-TGHSSSLDAR 64
      | | | | | : | | | | |
QY      41 -----PLHQAMRAAGDEFEFTRFRRTFSDLAQLHTPPGSAQORFTQVSDLELFOGGPNWG 94
      : | | | | | | | | | | : | | | | | : | | | | |
Db      65 EVIPMAAVKQALREAGDEFEFLRTRRAFSDLTSQHLHTPGTAYQSFQOVNLELFRDGVNWG 124
      | | | | | : | | | | | : | | | | | : | | | | |
QY      95 RLVAFFVFGALCAESVNKEMEPLVGQVQDMMVAYLETRLADWIHSSGGWAEFTALYGDG 154
      | : | | | | | | | | | : | | : | | | | | : | | | | |
Db      125 RIVAFSFGGALCVESVDKEMQVLSRIASWMATYLNHDHPWIQDNGGMDTFVELYGNM 184
      | : | | | | | | | | | : | | : | | | | | : | | | | |
QY      155 ALBEARRLRE--GNMASVRIVLTGAVALGAL 183
      | : | : | : | : | : | : | : | : | : | : | : |
Db      185 AAASRKGOERFNRMWELTGMTVAGVLLGSL 215
      | : | : | : | : | : | : | : | : | : | : | : |

```

RESULT 12  
US-10-659-705-7  
; Sequence 7, Application US/10659705  
; Publication No. US20040117867A1

Query Match	42.9%;	Score 432.5;	DB 16;	Length 229;
Best Local Similarity	41.7%;	Pred. No. 1.1e-36;		
Matches 95;	Conservative 22;	Mismatches 62;	Indels 49;	Gaps 4;

```
QY      11 RALVADFVGKYLRKGY-----VCAGAPGEGP-----          37
        | | | | | | | | : | : |
Db       6 RELVIDFSYKLSQRGHCMSELEEBEDENRTDTAAEAEMDSVLNGSPSWHPAGHVNGAT    65
                                                | | | | |
QY      38 -----AADPLHQAMRAGDEFETRFRRTFSDLAQLHVTPGSAQQRFTOVSDE    85
        : | : | | | | | : | | | | : | : | : | : | : | : |
Db       66 VHRSSLEVHEIVRASDVROALRDAGDEFELRYRAFSDLTSQLHTPTGTAYQSFEQVVNE   125
                                                | | | | |
QY      86 LFOGGPNWGRLVAFFVEFGALCAESVNKEMEPLVGQVQDDMMVAYLETRLADWIHSSGWA   145
        | | | | | | | | | | | | | | | | | | : | : | : | : |
Db      126 LFHDGVNMGRIVAFFSFGALCVESVDKEMRVLVGRIVSMWTYYLTDHLDPWIOENGWE   185
                                                | | | | |
QY     146 EFTALYGDGALEEARRLREGNMASVRTVLTCGAVALLGALVTYGAEFFASK    193
        | | | : | | : | | : | : | | | | : | : | : |
Db     186 RFVDLYGNNA---AAELRKGOETFNKKLLTGATVAGVLL-LGSLLSRK    229
```

RESULT 13  
US-10-792-517-2

```

; Sequence 2, Application US/10792517
; Publication No. US20040152179A1
; GENERAL INFORMATION:
; APPLICANT: Youle et al.
; TITLE OF INVENTION: RECEPTOR-MEDIATED UPTAKE OF AN EXTRACELLULAR BCL-XL
; TITLE OF INVENTION: FUSION PROTEIN INHIBITS APOPTOSIS
; FILE REFERENCE: 4239-55417
; CURRENT APPLICATION NUMBER: US/10/792,517
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/639,245
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/149,220
; PRIOR FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: genetic fusion
US-10-792-517-2

```

Query Match	42.9%;	Score	432.5;	DB	16;	Length	411;
Best Local Similarity	39.9%;	Pred. No.	2.4e-36;				
Matches	93;	Conservative	26;	Mismatches	63;	Indels	51;
						Gaps	4;

```

QY      11 PALVADFVGKYLRQKGY-----VCGAGP-----GEGPAA 39
      | | | | : | | | | |
Db      26 RELVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSMHLADSPAV 85
      | | | | : | | | | |
QY      40 D-----PLHQAMRAAGADEFETRFRRTFSDLLAQLHVTGPSAQQRPTQ 81
      : | | | | : | | | | | : | | | | : | | | |
Db      86 NGATAHSSSLDAREVIPAAMAVKQALREAGDEFELRYRRALFSDLLTSQLHITPGTAYQSFEO 145
      | | | | : | | | | | : | | | | : | | | |
QY      82 VSDFLFOGEPNWMGRLLVAFVFEFCALCAESVKNKEMEPLVGOQDMMVAYLETRLADWISS 141
      | : | | : | | | | | | | | | | | | : | | | | :
Db      146 VVNELFRDGVNMWGRIVAFSFGGALCVESVDKEMOVLVSRIAMMATYLLNDHLEPWIQEN 205
      | | | | : | | | | | : | | | | : | | | | :
QY      142 GGWAETALYGDGALLEEARRLRE--GNMWASVRTVLTGAVALGALVTVGAFPA 192
      | | | | : | | | | | : | | | | : | | | | :
Db      206 GGWDTFVELLYGNNAALAESRKQGERPNRMWFLTGMTVAGVLLGSLFSRKAYSA 258

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BCL2 proteins
US-10-659-705-7

```

```

Query Match          42.6%; Score 429.5; DB 15; Length 233;
Best Local Similarity 41.3%; Pred. No. 2.4e-36;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps

QY      11 RAIVADFVGKLRQKGY-----V 28
          | | | | | | | | | |
          | | | | | | | | | |
Db       6 RELAVDFLSYKLSQKGYSWSQFSDVEENRTEAPDEGTESERETPSAINGNPSWHLADSPAV 65

```

OY 29 CGAGPGEPPAD-----PLHQAMRAAGDEFEFTRFRRTFSDLAQLHTVTPGSAQQRFT 80  
DB 66 NGA-TGHSSSLDAREVIMAAVKQALREAGDEFLRYRAFSDLTSQHLTPGTAYQSFE 124  
OY 81 QVSDLEFQGGPNWGRLLVAFVFGAALCAESVKNKEMEPLVGQVQDMMVAYLETRLADWIHS 140  
DB 125 QVNNELFRDGVNWGRIVAFSFGALCVESVDKEMQVLVSRIASWMATYLNHDHLEPWIQD 184  
OY 141 SGGWAEFTALYDGALEEARLRE--GNWASVRTVLTGAVALLGAL 183  
DB 185 NGWDTFVELYGNNAAESRKQERFNRWFLTGMTVAGVLLGSL 229

RESULT 15

US-09-734-846-2  
; Sequence 2, Application US/09734846  
; Patent No. US20010007025A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Monté, Brett P.  
; APPLICANT: Nickoloff, Brian J.  
; APPLICANT: Zhang, QingQing  
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
; FILE REFERENCE: ISPH-0528  
; CURRENT APPLICATION NUMBER: US/09/734,846  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 09/277,020  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 09/167,921  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 09/323,743  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-734-846-2

Query Match 42.4%; Score 427.5; DB 9; Length 233;  
Best Local Similarity 40.6%; Pred. No. 3.8e-36;  
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

OY 11 RALVADFGYKLRQKGY-----VCGAGP-----GEGPAA 39  
DB 6 RELVVDPLSLYKLSQKYSWSQFSDVEENRTPEAGTESEMETPSALINGNPSWHLADSPAV 65  
OY 40 D-----PLHQAMRAAGDEFEFTRFRRTFSDLAQLHTVTPGSAQQRFTQ 81  
DB 66 NGATAHSSSLDAREVIMAAVKQALREAGDEFLRYRAFSDLTSQHLTPGTAYQSFEQ 125  
OY 82 VSDELFOGGPNWGRLLVAFVFGAALCAESVKNKEMEPLVGQVQDMMVAYLETRLADWIHS 141  
DB 126 VVNNELFRDGVNWGRIVAFSFGALCVESVDKEMQVLVSRIASWMATYLNHDHLEPWIQEN 185  
OY 142 GGWAEFTALYDGALEEARLRE--GNWASVRTVLTGAVALLGAL 183  
DB 186 GGWDTFVELYGNNAAESRKQERFNRWFLTGMTVAGVLLGSL 229

Search completed: April 10, 2005, 22:59:28  
Job time : 228.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2005, 22:09:08 ; Search time 17 Seconds  
(without alignments)  
1092.343 Million cell updates/sec

Title: US-09-925-674B-9

Perfect score: 1009

Sequence: 1 MATPASTPDTRALVADFVG.....LTGAVALGALVTGAFPAK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapexc 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	428.5	42.5	233	2	I49056	bcl-x long - mouse
2	427.5	42.4	233	2	B47537	apoptosis regulato
3	424.5	42.1	233	2	S51761	BCL-X protein - ra
4	423.5	42.0	233	2	A37332	transforming prote
5	414	41.0	232	2	S24390	transforming prote
6	411.5	40.8	239	1	TVHUA1	transforming prote
7	411	40.7	236	2	I67432	BCL-2 - rat (fragm
8	406	40.2	236	2	I53744	gene bcl-2 protein
9	405	40.1	236	1	TVMSA1	transforming prote
10	404.5	40.1	233	2	I67431	BCL-X-Long - rat
11	402	39.8	236	2	JC7383	B-cell lymphoma 2
12	378	37.5	190	2	A47537	apoptosis regulato
13	377.5	37.4	214	2	I49057	bcl-x transmembran
14	374.5	37.1	227	2	JB0203	apoptosis regulato
15	356	35.3	216	2	B37332	transforming prote
16	348.5	34.5	199	1	TVMSB1	transforming prote
17	345	34.2	205	1	TVHUB1	transforming prote
18	277.5	27.5	154	2	I58194	gene bcl-2 protein
19	182	18.0	170	2	I49055	bcl-x short - mous
20	174	17.2	176	2	I67435	gene bcl-xshort pr
21	171	16.9	211	2	S58873	Bak protein - huma
22	168	16.7	211	2	S58875	cdn-2 protein - hu
23	158.5	15.7	192	2	D47538	bcl-2-associated p
24	154	15.3	192	2	A47538	bcl-2-associated p
25	151	15.0	261	2	H88578	protein ced-9 [imp
26	151	15.0	280	2	A53189	apoptosis suppress
27	150.5	14.9	133	2	I53295	bcl-2-associated p
28	147.5	14.6	179	2	JC7255	Bax-delta protein
29	147.5	14.6	218	2	B47538	bcl-2-associated p

30	142	14.1	177	2	S54778	NR-13 protein - qu
31	138.5	13.7	143	2	I38921	bcl-2-associated p
32	138	13.7	255	2	JC7567	Mcl-1a protein - 2
33	116	11.5	175	2	I39055	Bcl-2 related - hu
34	116	11.5	350	2	A47476	BCL2 homolog MCL1
35	105	10.4	172	2	I49449	hemopoietic-specif
36	88	8.7	185	2	B83217	hypothetical prote
37	87	8.6	3433	1	GNWVKV	genome polypeptid
38	86.5	8.6	301	2	T36534	probable lipase/es
39	86	8.5	270	2	A12598	dihydrodipicolinat
40	86	8.5	279	2	B97381	dihydrodipicolinat
41	84.5	8.4	358	1	AJLCOB	glutamate-ammonia
42	83.5	8.3	872	2	H95160	alanyl-tRNA synthe
43	83.5	8.3	872	2	G98026	alanine-tRNA ligas
44	83	8.2	3430	1	GNWVMV	genome polypeptid
45	81.5	8.1	886	2	A32758	beta-amyloid-like

ALIGNMENTS

RESULT 1  
I49056  
bcl-x long - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C/Accession: I49056; S52866  
R/Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A/Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
A/Reference number: I49055; MUID:95052604; PMID:7963517  
A/Accession: I49056  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-233 <RBS>  
A/Cross-references: UNIPROT:Q64373; EMBL:U10101; NID:g506647; PIDN:AAA82173.1; PID:g5066  
R/Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.  
submitted to the EMBL Data Library, November 1994  
A/Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line throug  
A/Reference number: S52866  
A/Accession: S52866  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-233 <RMS>  
A/Cross-references: EMBL:X83574; NID:g695622; PIDN:CAA58557.1; PID:g695623  
C/Superfamily: bcl apoptosis regulator, inhibitory type  
Query Match 42.5%; Score 428.5; DB 2; Length 233;  
Best local Similarity 41.3%; Pred. No. 1.8e-32;  
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;  
QY 11 RALVADFVGYKLRQKG-----V 28  
Db 6 RELVDFLSYKLSQKGYSWSQPSDVEENRTAPEETEARETSPAINGNPSMHLADSPAV 65  
QY 29 CGAGPGEGBPAD-----PLHQAMRAAGDEFETRFRRTSPDLAAQLHVTGPSAQORFT 80  
Db 66 NGA-TGHSSSLDAREVTPMAAVKQALREAGDEFELRYRRAFSDLTSQ LHITPGTAYQSFE 124  
QY 81 QVSDLEFGQGPNNWRLVAFVFGALCAESVNKEMEPLVGQVQDMVAVYLETRLADWIHS 140  
Db 125 QVNVNELFRDGVNMGRIVAFSPFGALCVESVDKEMQVLVSRIASWMATYLLNDHLEPWIQE 184  
QY 141 SGGWAEFTALYGDALBEARLR--GNWASVRTVLTGAVALGAL 183  
Db 185 NGGWDFFVDLYGNNAABSRKQGERFNRWFLTGMTVAGVLLGSL 229  
RESULT 2  
B47537  
apoptosis regulator bcl-xl - human  
N/Alternate names: bcl-2-related protein  
N/Contains: apoptosis regulator bcl-xs

C;Species: Homo sapiens (man)  
C;Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: B47537; C47537  
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;  
Cell 74, 597-608, 1993  
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic  
A;Reference number: A47537; MUID:93364977; PMID:8358789  
A;Accession: B47537  
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-233 <BOI>  
A;Cross-references: UNIPROT:Q07817; GB:L20121; NID:g510900; PIDN:CAA80661.1; PID:g510901  
A;Accession: C47537  
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-69, 'G', 71-125, 189-233 <BO2>  
A;Cross-references: GB:L20122; NID:g623236; PIDN:CAA80662.1; PID:g623237  
C;Genetics:  
A;Gene: GDB:BCR2L  
A;Cross-references: GDB:228079  
C;Superfamily: bcl apoptosis regulator, inhibitory type  
C;Keywords: alternative splicing; apoptosis  
F;1-233/Product: apoptosis regulator bcl-xl #status predicted <MAT>  
F;1-125,189-233/Product: apoptosis regulator bcl-xs #status predicted <MA2>

Query Match 42.4%; Score 427.5; DB 2; Length 233;  
Best Local Similarity 40.6%; Pred. No. 2.2e-32;  
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADFVGYKLRQKGY-----VCGAGP---GEGPAA 39  
Db 6 RELVDFLSYKLSQKGYWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65  
QY 40 D-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTGPSAQORFTQ 81  
Db 66 NGATAHSSSLDAREVTPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTTGTAYQSFEQ 125  
QY 82 VSDELFOGPPNMGRLVAFVFGAALCAESVNKEMEPLVGQVQDMMVAYLETRLADWIHSS 141  
Db 126 VVNELFRDGVNMGRIIVAFSFGALCVESVDKEMQVLVSRIAAWMATYTLNDHLEPWIQEN 185  
QY 142 GWAFFETALYGDGALBEARRLRE--GNWASVRTVLTGAVALGAL 183  
Db 186 GGWDTFVELYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 3

BCL-X protein - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C;Accession: S51761; S51762  
R;Michaelidis, T.M.

submitted to the EMBL Data Library, November 1994  
A;Reference number: S51761

A;Accession: S51761

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-233 <MIC>

A;Cross-references: UNIPROT:P53563; EMBL:X82537; NID:g607176; PIDN:CAA57886.1; PID:g607171  
A;Experimental source: embryonic; brain

A;Accession: S51762

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-125, 189-233 <MI2>

A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57887.1; PID:g607178  
A;Experimental source: embryonic; brain

A;Note: smaller form due to splicing

C;Genetics:

A;Introns: 125/3

C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 42.1%; Score 424.5; DB 2; Length 233;

Best Local Similarity 41.3%; Pred. No. 4.1e-32;  
Matches 92; Conservative 22; Mismatches 56; Indels 53; Gaps 4;  
QY 13 LVADFVGYKLRQKGY-----VCG 30  
Db 8 LVDFLSYKLSQKGYWSQFSDVEENRTEAPEETPERETPSAINGNPSWHLADSPAVNG 67  
QY 31 AGPEGEPAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTGPSAQORFTQV 82  
Db 68 A-TGHSSSLDAREVTPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTTGTAYQSFEQV 126  
QY 83 SDELFOGPPNMGRLVAFVFGAALCAESVNKEMEPLVGQVQDMMVAYLETRLADWIHSSG 142  
Db 127 VNELFRDGVNMGRIIVAFSFGALCVESVDKEMQVLVSRIASWMATYTLNDHLEPWIQENG 186  
QY 143 GWAFFETALYGDGALBEARRLRE--GNWASVRTVLTGAVALGAL 183  
Db 187 GGWDTFVDLYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 4

A37332

transforming protein (bcl-2-alpha) - chicken

C;Species: Gallus gallus (chicken)

C;Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 09-Jul-2004  
C;Accession: A37332; S35453

R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992  
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vari

A;Reference number: A37332; MUID:92375724; PMID:1508712

A;Accession: A37332

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-233 <EGU>

A;Cross-references: UNIPROT:Q00709; EMBL:D11381

C;Genetics:

A;Introns: 189/3

C;Superfamily: bcl apoptosis regulator, inhibitory type

C;Keywords: mitochondrion; transforming protein; transmembrane protein

Query Match 42.0%; Score 423.5; DB 2; Length 233;  
Best Local Similarity 38.0%; Pred. No. 5.1e-32;  
Matches 87; Conservative 32; Mismatches 61; Indels 49; Gaps 4;

QY 9 DTRALVADFVGYKLRQKGYVCGAG-----PGEPPADP----- 41  
Db 10 DNREIVLKVIHYKLSQKGYDWAAGEDRPVPAPAPAPAAVAAGASSHHRRPEPPGSA 69  
QY 42 -----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTGPSAQORFTQVSD 84  
Db 70 AASEVPPAEGRLRAPPGVHLLRQAGDEFSRRYQRDFAQNSQGLHTPTTAHGRVAVVE 129  
QY 85 ELFOGPPNMGRLVAFVFGAALCAESVNKEMEPLVGQVQDMMVAYLETRLADWIHSSG 144  
Db 130 ELFRDGVNMGRIIVAFSFGALCVESVNREMSPLVDNIATWMTETLNRHLHNTIQDNGW 189  
QY 145 AEFTALYGDGALBEARRLREGNWSVRTVLTGAVALGALVTGAFPAK 193  
Db 190 DAFVELYGN-----SMRPLFDFTSWISLTKTILS-LVLVGACITTLGAYLGHK 233

RESULT 5

S24390

transforming protein (bcl-2) homolog - chicken

C;Species: Gallus gallus (chicken)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S24390

R;Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.

Biochim. Biophys. Acta 1132, 109-113, 1992  
A;Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue c

A;Reference number: S24390; MUID:92379084; PMID:1511008

A;Accession: S24390

A;Status: preliminary



RESULT 8  
153744  
gene bcl-2 protein - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C/Accession: 153744  
R/Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.  
Gene 140, 291-292, 1994  
A/Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.  
A/Reference number: 153744; MUID:94193015; PMID:8144041  
A/Accession: 153744  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-236 <RES>  
A/Cross-references: UNIPROT:P49950; GB:L14680; NID:g408946; PIDN:AAA53662.1; PID:g408947  
C/Genetics:  
A/Gene: bcl-2  
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 40.2%; Score 406; DB 2; Length 236;  
Best Local Similarity 35.8%; Pred. No. 2.2e-30;  
Matches 83; Conservative 34; Mismatches 63; Indels 52; Gaps 3;  
QY 9 DTRALVADFVGYKLRQKGY-----PG----- 27  
Db 10 DNREIVMKYIHYKLSQRGYEMDGTDEDSAPLRAAPTPGIFSPQESNKPAPVHRDTAART 69  
QY 28 -----VCGAGPGEPAADPLHQAMRAAGDEFETRFRRTFSDLAQLHVTGPSAQQRFTQ 81  
Db 70 SPLRPLVANAGPALSPVPSPVHLLTRAGDDFSRRYRDFEAMSSQLHLLPTFARGRPAT 129  
QY 82 VSDELFOGPGPNWGRLLVAFVFGAALCAESVKNKEMEPVLVGQVQDMVVAYLETRLADWIHSS 141  
Db 130 VVEELFRDGVNWGRIVAFEFEGVGCVSVNREMSPLVDNIALMWTXYLNRHLHTWIQDN 189  
QY 142 GGMAEFTALYGDGALBEARRLREGNMAVSRTVLTGAVALGALVTGAFPAASK 193  
Db 190 GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSL-LPWVGACITLGAYLGHK 236

RESULT 9  
TVMSAI  
transforming protein bcl-2-alpha - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 28-Jul-2003  
C/Accession: A25960; E37332  
R/Negrini, M.; Siliini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.  
Cell 49, 455-463, 1987  
A/Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homolog  
A/Reference number: A90893; MUID:87187643; PMID:3032455  
A/Accession: A25960  
A/Molecule type: DNA  
A/Residues: 1-236 <NEG>  
A/Cross-references: GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1; PID:g387109  
R/Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res. 20, 4187-4192, 1992  
A/Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety  
A/Reference number: A37332; MUID:92375724; PMID:1508712  
A/Accession: E37332  
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A/Molecule type: DNA  
A/Residues: 1-33,'E',34-220,'AL',223-236 <EGU>  
C/Genetics:  
A/Gene: BCL2  
A/Intons: 192/3  
C/Superfamily: bcl apoptosis regulator, inhibitory type  
C/Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane pro

Query Match 40.1%; Score 405; DB 1; Length 236;  
Best Local Similarity 37.1%; Pred. No. 2.8e-30;  
Matches 86; Conservative 33; Mismatches 61; Indels 52; Gaps 5;

QY 9 DTRALVADFVGYKLRQKGYCGAG-----PG----- 34  
Db 10 DNREIVMKYIHYKLSQRGYEMDAGDADAAPLGAAPTPGIFSPQESNMPAVHREMAART 69  
QY 35 -----EGPAADP-----LHQAMRAAGDEFETRFRRTFSDLAQLHVTGPSAQQRFTQ 81  
Db 70 SPLRPLVATAGPALSPVPCVHLLTRAGDDFSRRYRDFEAMSSQLHLLPTFARGRPAT 129  
QY 82 VSDELFOGPGPNWGRLLVAFVFGAALCAESVKNKEMEPVLVGQVQDMVVAYLETRLADWIHSS 141  
Db 130 VVEELFRDGVNWGRIVAFEFEGVGCVSVNREMSPLVDNIALMWTXYLNRHLHTWIQDN 189  
QY 142 GGMAEFTALYGDGALBEARRLREGNMAVSRTVLTGAVALGALVTGAFPAASK 193  
Db 190 GGWDAFVELYG----PSMRPLFDFSWLSLKTLLS-LPWVGACITLGAYLGHK 236

RESULT 10  
167431  
BCL-X-Long - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C/Accession: 167431  
R/Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.  
Endocrinology 136, 232-241, 1995  
A/Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equine  
onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.  
A/Reference number: 153295; MUID:95129487; PMID:7828536  
A/Accession: 167431  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-233 <RES>  
A/Cross-references: UNIPROT:P53563; EMBL:U34963; NID:g1004376; PIDN:AAA77686.1; PID:g1004  
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 40.1%; Score 404.5; DB 2; Length 233;  
Best Local Similarity 39.6%; Pred. No. 3e-30;  
Matches 89; Conservative 22; Mismatches 61; Indels 53; Gaps 4;  
QY 11 RALVADFVGYKLRQKGY-----V 28  
Db 6 RELVDFLSYKLSQKGYSWSQFSDVEENRTAPETEPERETPSAINGNSWHLADSPAV 65  
QY 29 CGAGPGEPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAQLHVTGPSAQQRFT 80  
Db 66 NGA-TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPGTVYQSF 124  
QY 81 QVSDELFOGPGPNWGRLLVAFVFGAALCAESVKNKEMEPVLVGQVQDMVVAYLETRLADWIHSS 140  
Db 125 QVNEELFRDGVNWGRIVASSFGALCVESVDKEMQVLVSRIASWATYLNHLEPWIQ 184  
QY 141 SGMAEFTALYGDGALBEARRLREGNMAVSRTVLTGAVALGAL 183  
Db 185 NGGMDTFVDLYGNNTAPESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 11  
JC7383  
B-cell lymphoma 2 protein - Chinese hamster  
C/Species: Cricetulus griseus (Chinese hamster)  
C/Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 09-Jul-2004  
C/Accession: JC7383  
R/Tomicic, M.T.; Christmann, M.; Kaina, B.  
Biochem. Biophys. Res. Commun. 275, 899-903, 2000  
A/Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.  
A/Reference number: JC7383  
A/Contents: Ovary  
A/Accession: JC7383  
A/Molecule type: mRNA  
A/Residues: 1-236 <TOM>  
A/Cross-references: UNIPROT:Q9JUV8; GB:AJ271720  
C/Comment: This protein has anti-apoptotic function, and supports cell survival.





**B37332**

transforming protein (bcl-2-beta) - chicken

C; Species: Gallus gallus (chicken)

C:/Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 28-Jul-2003  
C:/Accession: B17332.1 S25453

C:\Accession: B37332; S35452

R; Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A/Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues

A;Accession: B37332  
A;Reference number: A37332; MUID:92375724; PMID:1508712

A;Status: nucleic a

A: molecule type: DNA

A;Residues: 1-216 <EGU>

A; Cross-references: EMB

C/Superfamily: bcl apoptosis regulator, inh1

Query Match	35 38: 60000 355: nm 2
	1 22

Query Match  
Best Local

Matches 71; Conservative 21; Mismatches 49; Indels

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1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

QY 9 DTRALVADFGYKLRQKGYVCGAG-----PGEGRADP----- 41

Db 10 DNREIVLKYIHYKLSQRGYDWAAGEDRPVPVPAPAPAAAPAAVAAGAASSHHRPEPPGSA 69

42 -----LHQAMRAAGDEFETRFRRTFSDLAQLHVTPGSAQQRFTQVSD 84

D6 70 AASEVPPAEGLRPAPGVHLALRQAGDEFSSRYQRDFAQMSGQLHTPTAHGRFVAVVE 129

85 ELFOGGPNTWGR LVAFVFGAALCAESVNKEMEPLVGQVQDMMVAYLETRLADWTHSSGGM 144

130 ELFRDGVNWGRIVAFEEFGVMCVESVNREMSPLVDNIATWMTXYLNRHLHWIQDNGGW 189

QY \* 145 AEF7A 149

Db 190 VRACA 194

Search completed: April 10, 2005, 22:44:41  
Job time : 17 secs

Job time : 17 secs